

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 20:51:16 ; Search time 2057.56 Seconds
(without alignments)
12719.092 Million cell updates/sec

Title: US-10-764-316-5
Perfect score: 468
Sequence: 1 tgaataataatggaacacac.....tggatgattgcaggagattt 468

Scoring table: OLIGO NUC
GAPOP 60.0 , Gapext 60.0

Searched: 48236798 seqs, 2795965780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_est7:*
- 7: gb_est8:*
- 8: gb_est9:*
- 9: gb_est10:*
- 10: gb_est11:*
- 11: gb_est12:*
- 12: gb_est13:*
- 13: gb_est14:*
- 14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	21	4.5	627	13	CW375149	CW375149 fabb001f0
C 2	21	4.5	649	13	CW258112	CW258112 104 723 1
C 3	21	4.5	682	13	CW375148	CW375148 fabb001f0
C 4	21	4.5	983	14	CT013281	CT013281 KBRH12111
C 5	21	4.5	999	14	DU750205	DU750205 ASNFI346.
C 6	21	4.5	1217	12	CC314499	CC314499 TAM32-17E
C 7	20	4.3	245	13	CL219260	CL219260 ZMMWBC042
C 8	20	4.3	611	14	DX327753	DX327753 OR_ABa024
C 9	20	4.3	613	9	CX687527	CX687527 ydd80c08.
C 10	20	4.3	626	9	CX688942	CX688942 yde22f05.
C 11	20	4.3	640	10	DT673917	DT673917 s13dtr65C
C 12	20	4.3	679	11	BH557567	BH557567 BOGO92TF
C 13	20	4.3	785	11	BZ162280	BZ162280 CH230-276
C 14	20	4.3	896	3	BU795670	BU795670 SJF2DUA01
C 15	19	4.1	230	7	B3212456	B3212456 BB212456
C 16	19	4.1	281	7	B3369985	B3369985 BB369985
C 17	19	4.1	288	3	BQ803876	BQ803876 WHE2843.B
C 18	19	4.1	415	2	BG264482	BG264482 daa82f12.
C 19	19	4.1	422	12	CC812860	CC812860 ZMMWBC052

20	19	4.1	427	11	BH752910	BH752910
C 21	19	4.1	428	11	AQ514846	AQ514846
C 22	19	4.1	437	8	CN184594	CN184594
C 23	19	4.1	451	11	BZ379446	BZ379446
C 24	19	4.1	458	7	AW680443	AW680443
C 25	19	4.1	468	9	CX538294	CX538294
C 26	19	4.1	478	11	AQ130921	AQ130921
C 27	19	4.1	483	10	DV773477	DV773477
C 28	19	4.1	492	14	CR900936	CR900936
C 29	19	4.1	522	7	BE429624	BE429624
C 30	19	4.1	549	2	BM136116	BM136116
C 31	19	4.1	558	13	CZ891688	CZ891688
C 32	19	4.1	561	13	CW484121	CW484121
C 33	19	4.1	567	4	CA639214	CA639214
C 34	19	4.1	577	4	CB085812	CB085812
C 35	19	4.1	577	14	DX171753	DX171753
C 36	19	4.1	577	14	CR488931	CR488931
C 37	19	4.1	578	3	BQ400766	BQ400766
C 38	19	4.1	579	11	AZ704872	AZ704872
C 39	19	4.1	587	12	CE742874	CE742874
C 40	19	4.1	595	11	AZ704151	AZ704151
C 41	19	4.1	600	14	DX172123	DX172123
C 42	19	4.1	617	13	DU224130	DU224130
C 43	19	4.1	619	7	AW641002	AW641002
C 44	19	4.1	624	7	BE492287	BE492287
C 45	19	4.1	624	12	CE178051	CE178051

ALIGNMENTS

RESULT 1

CW375149/c

LOCUS

DEFINITION

Sorghum bicolor genomic clone fabb001f052g07, genomic survey

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

CONTACT

ORION GENOMICS, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6379

Fax: 314 615 6375

Email: jbedell@oriongenomics.com

Plate: fabb001f052 row: g column: 07

Seq primer: k Reverse

Class: methylation filtered

High quality sequence stop: 627.

Location/Qualifiers

1. 627

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/cultivar="ATx623"

/db_xref="taxon:4558"

/clone="fabb001f052g07"

/clone_lib="Sorghum methylation filtered library (LibID: 104)"

Mon Nov 6 11:55:55 2006

```

/notes="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
Query Match          4.5%; Score 21; DB 13; Length 627;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAATAAATAATGGAACACACA 21
|||||
Db 467 TGAATAAATAATGGAACACACA 447

RESULT 2
CW258112/c
LOCUS
DEFINITION
104 723 11227699.116 35158.066 Sorghum methylation filtered library
(LiBiD: 104) Sorghum bicolor genomic clone 11227699, genomic survey
sequence.
CW258112
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum bicolor (sorghum)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 649)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddalo, J.A. and
Martensen, R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 723 row: 0 column: 19
Seq primer: F3 Reverse
Class: methylation filtered
High quality sequence stop: 649.
Location/Qualifiers
1. 649
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11227699"
/clone_lib="Sorghum methylation filtered library (LiBiD:
104)"
/notes="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
Query Match          4.5%; Score 21; DB 13; Length 649;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAATAAATAATGGAACACACA 21
|||||
Db 467 TGAATAAATAATGGAACACACA 447

RESULT 3
CW375148
LOCUS
DEFINITION
682 bp DNA linear GSS 01-NOV-2004
fabb001f052g07f0 Sorghum methylation filtered library (LiBiD: 104)
Sorghum bicolor genomic clone fabb001f052g07, genomic survey
sequence.
CW375148
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum bicolor (sorghum)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 682)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddalo, J.A. and
Martensen, R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: fabb001f052 row: 5 column: 07
Seq primer: f Forward
Class: methylation filtered
High quality sequence stop: 682.
Location/Qualifiers
1. 682
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="fabb001f052g07"
/clone_lib="Sorghum methylation filtered library (LiBiD:
104)"
/notes="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
Query Match          4.5%; Score 21; DB 13; Length 682;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAATAAATAATGGAACACACA 21
|||||
Db 477 TGAATAAATAATGGAACACACA 497

RESULT 4
CT013281/c
LOCUS
DEFINITION
983 bp DNA linear GSS 09-AUG-2005
KBRH121117 genomic clone, KBRH (HindIII) BAC library Brassica rapa
subsp. pekinensis, genomic survey sequence.
CT013281
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Viehöver, P., Holtgraewe, D. and Weisshaar, B.
BAC end sequences of Brassica rapa
Unpublished

2 (bases 1 to 983)
Li, Y. and Weisshaar, B.
Direct Submission

Submitted (09-AUG-2005) Weisshaar B., Bielefeld University,
Institute for Genome Research, Universitätsstrasse 25, D-33594
Bielefeld, Germany

Contact: Bernd Weisshaar

Bielefeld University, Institute for Genome Research
Universitätsstrasse 25, D-33594 Bielefeld, Germany Email:
bernd.weisshaar@uni-bielefeld.de

BAC end sequences of Brassica rapa BAC clone KBRH121117; generated
as contribution to the 'Multinational Brassica rapa Sequencing
Project'. Seq primer: sp6B ATTAGGTGACATATAG

Class: BAC ends.

FEATURES
source

1..983
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/strain="Chifu type 401-42"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRH121117"
/clone_lib="KBRH, Brassica rapa HindIII BAC library
GF-SCF-1002, Vector: pCUGIbac1"
/lab_host="E.coli DH10B"

ORIGIN

Query Match 4.5%; Score 21; DB 14; Length 983;

Best Local Similarity 100.0%; Pred. No. 7.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 324 TTGGTAATGATGTTTCTTCT 344
|||||
Db 821 TTGGTAATGATGTTTCTTCT 801
|||||

RESULT 5
DU750205

LOCUS 999 bp DNA linear GSS 27-JAN-2006
DEFINITION ASNF1346.g2 HF130_10-06-02 uncultured marine microorganism
HF130_10-06-02 genomic clone HF0130_014B01, genomic survey
sequence.

ACCESSION DU750205.1 GI:85760041
VERSION DU750205
KEYWORDS GSS.

SOURCE uncultured marine microorganism HF130_10-06-02
ORGANISM uncultured marine microorganism HF130_10-06-02
unclassified sequences; environmental samples.

REFERENCE 1 (bases 1 to 999)

DeLong, E.P., Preston, C.M., Mincer, T., Rich, V., Hallam, S.J.,
Frigaard, N.U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S.W.
and Karl, D.M.

Comparative genomics reveals ecological trends in stratified
microbial communities in the ocean's interior

Science (2006) In press

Contact: Susan Lucas, Alex Copeland, Sam Pittluck, Alla Lapidus,
Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson
and Edward DeLong

US DOE Joint Genome Institute

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2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

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Email: PWRichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6

um, greater than 0.22 um fraction. Sample Date: 10/6/2002
Coordinates: 22.45 N, 158 W Depth 130 m Temperature: 22.19 C
Salinity: 35.31 psu Oxygen: 204.9 umol/kg
Class: fosmid ends.

FEATURES
source

Location/Qualifiers
1..999
/organism="uncultured marine microorganism HF130_10-06-02"
/mol_type="genomic DNA"
/db_xref="taxon:361146"
/clone="HF0130_014B01"
/cell_type="marine picoplankton, less than 1.8 um, greater
than 0.22 um fraction"
/clone_lib="HF130_10-06-02"
/note="Vector: pC1FOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 130 m
depth on 10/6/2002, Coordinates: 22.45 N, 158 W. Sample
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 130 m
Temperature: 22.19 C Salinity: 35.31 psu Oxygen: 204.9
umol/kg"

ORIGIN

Query Match 4.5%; Score 21; DB 14; Length 999;

Best Local Similarity 100.0%; Pred. No. 7.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 254 AGAAGACTGATGAGTGATT 274
|||||
Db 261 AGAAGACTGATGAGTGATT 281
|||||

RESULT 6

CC314499/c

LOCUS CC314499 1217 bp DNA linear GSS 14-MAY-2003
DEFINITION TAM32-17E11_EC1.1 TAM32 Gallus gallus genomic clone TAM32-17E11,
genomic survey sequence.

ACCESSION CC314499.1 GI:30708554

VERSION GSS

KEYWORDS Gallus gallus (chicken)

SOURCE Gallus gallus

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 1217)

Kremitzki, C., Higginbotham, J., Wyllie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Mardis, E. and Wilson, R.

Gallus gallus BAC End Reads

Unpublished (2003)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 152000 Std Error: 0.00

Seq primer: EC1 TAGACTCACTATAGGCG

Class: BAC ends

High quality sequence start: 19

High quality sequence stop: 763.

FEATURES
source

Location/Qualifiers
1..1217
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="TAM32-17E11"
/sex="female"
/cell_line="UCD001, inbred 256"
/clone_lib="TAM32"

/note="Vector: pECBAC1; Site_1: EcoRI; Site_2: EcoRI;

TAM32 Female Chicken library - for library and clone

ordering information: http://www.hbz.tamu.edu"

ORIGIN

Mon Nov 6 11:55:55 2006

```

Query Match      4.5%; Score 21; DB 12; Length 1217;
Best Local Similarity 100.0%; Pred. No. 7.3; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 TGAAATTAATGGACACACA 21
Db 715 TGAAATTAATGGACACACA 695

RESULT 7
CL219260      245 bp DNA linear GSS 08-JAN-2004
LOCUS ZMWBBC0429L12f ZMWBBC Zea mays genomic clone ZMWBBC0429L12 5',
DEFINITION genomic survey sequence.
ACCESSION CL219260
VERSION CL219260.1 GI:40751934
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 245)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PGIR (2003c)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: Bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .245
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMWBBC0429L12"
/lab_host="E. coli DH10B"
/clone_lib="ZMWBBC"
/notes="vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"

ORIGIN
Query Match      4.3%; Score 20; DB 13; Length 245;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 TCACACAGACGCTGATGA 267
Db 2 TCACACAGACGCTGATGA 21

RESULT 8
DX327753/c      611 bp DNA linear GSS 20-JAN-2006
LOCUS OR_ABA0248005.r OR_ABA Oryza ridleyi genomic clone OR_ABA0248005
DEFINITION 3', genomic survey sequence.
ACCESSION DX327753
VERSION DX327753.1 GI:85604539
KEYWORDS GSS.
SOURCE Oryza ridleyi
ORGANISM Oryza ridleyi
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 611)

AUTHORS Kim,H., Collura,K., Wissoteki,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
TITLE Oryza Map Alignment Project)- Arizona Genomics Institute
JOURNAL OMAP (Unpublished (2005))
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 0248 row: 0 column: 05
Class: BAC ends.

FEATURES
Location/Qualifiers
1. .611
/organism="Oryza ridleyi"
/mol_type="genomic DNA"
/db_xref="taxon:83308"
/clone="OR_ABA0248005"
/tissue_type="leaves"
/lab_host="DH10B"
/clone_lib="OR_ABA"
/notes="vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      4.3%; Score 20; DB 14; Length 611;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 TGTTCCTCTCAACCCATG 353
Db 264 TGTTCCTCTCAACCCATG 245

RESULT 9
CX687527      613 bp mRNA linear EST 19-JAN-2005
LOCUS ydd80c08.y2 Sea urchin EST Lib1 stronglycentrotus purpuratus cDNA
DEFINITION clone ydd80c08 5', mRNA sequence.
ACCESSION CX687527
VERSION CX687527.1 GI:57948974
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidae; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 613)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RPP01
High quality sequence stop: 613.

FEATURES
Location/Qualifiers
1. .613
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="ydd80c08"
/lab_host="DH10B"
/clone_lib="Sea urchin EST Lib1"

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/note="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: Not1;
Site 2: Sma1; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMVSPORT6.1 (Invitrogen)."

ORIGIN

Query Match 4.3%; Score 20; DB 9; Length 613;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 ACGTTGACTGACGCGAGAATT 120
|||||
Db 502 ACGTTGACTGACGCGAGAATT 521

RESULT 10

CX688942 626 bp mRNA linear EST 19-JAN-2005
LOCUS yde22f05.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
DEFINITION clone yde22f05 5', mRNA sequence.
ACCESSION CX688942
VERSION EST.
KEYWORDS Strongylocentrotus purpuratus
SOURCE Strongylocentrotus purpuratus

ORGANISM

Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.

REFERENCE

1 (bases 1 to 626)
Coffman, J.A., Robertson, A.J., Clifton, S., Pape, D., Hillier, L.,
Martins, J., Wylie, T., Dante, M., Meyer, R., Theising, B., Bowers, Y.,
Gibbons, M., Ronko, I., Tsagarelshvili, R., Ritter, E., Kennedy, S. and
Wilson, R.

TITLE

WashU Sea Urchin EST Project
Unpublished (2004)
Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

COMMENT

Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28Rppot
High quality sequence stop: 626.

FEATURES

source
1..626
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="yde22f05"
/lab_host="DH10B"
/clone_lib="Sea urchin EST Lib1"
/note="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: Not1;
Site 2: Sma1; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMVSPORT6.1 (Invitrogen)."

ORIGIN

Query Match 4.3%; Score 20; DB 9; Length 626;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 ACGTTGACTGACGCGAGAATT 120
|||||
Db 478 ACGTTGACTGACGCGAGAATT 497

RESULT 11

DT673917/c 640 bp mRNA linear EST 09-SEP-2005
LOCUS DT673917

DEFINITION

s13dLT65C12PM098 505552 Darnel ryegrass, Lolium temulentum L.,
Floral meristem Lolium temulentum cDNA, mRNA sequence.

ACCESSION

DT673917

VERSION

DT673917.1 GI:74338096

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..640

/organism="Lolium temulentum"

/mol_type="mRNA"

/db_xref="taxon:34176"

/tissue_type="Floral meristem"

/dev_stage="Six-week-old"

/clone_lib="Darnel ryegrass, Lolium temulentum L., Floral meristem"

/notes="Vector: Lambda Zap; Floral meristems of Darnel ryegrass, Lolium temulentum L. were isolated from greenhouse plants four days after long-day treatment. The plants were initially grown at short-day conditions for six weeks before the long day treatment. mRNAs were isolated from floral meristems and used for cDNA library construction."

ORIGIN

Query Match 4.3%; Score 20; DB 10; Length 640;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 TTTTTCAGTTCTTCAACAGA 418
|||||

Db 302 TTTTTCAGTTCTTCAACAGA 283
|||||

RESULT 12

BH557567/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Other_GSSs: BOGOG92TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

BH557567

BOGOG92TR

survey sequence.

BH557567

BH557567.1

GSS.

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 679)

Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)

15805490

Other_GSSs: BOGOG92TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

/note="vector: PTABAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SnHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN

Query Match 4.3%; Score 20; DB 11; Length 785;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 GGTTCAGGAGGAGGGGCGAG 86
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Db 206 GGTTCAGGAGGAGGGGCGAG 187
|||||

RESULT 14

BU795670 896 bp mRNA linear EST 23-OCT-2003
SJF2DUA01 SJF Schistosoma japonicum cDNA, mRNA sequence.

ACCESSION BU795670

VERSION BU795670.1 GI:28352677

KEYWORDS EST.

SOURCE Schistosoma japonicum

ORGANISM Schistosoma japonicum

REFERENCE 1 (bases 1 to 896)

AUTHORS Hu, W., Yan, Q., Shen, D.K., Liu, F., Zhu, Z.D., Song, H.D., Xu, X.R.,

Wang, Z.J., Rong, Y.P., Zeng, L.C., Wu, J., Zhang, X., Wang, J.J.,

Xu, X.N., Wang, S.Y., Fu, G., Zhang, X.L., Wang, Z.Q., Brindley, P.J.,

McManus, D.P., Xue, C.L., Peng, Z., Chen, Z. and Han, Z.G.

Evolutionary and biomedical implications of a Schistosoma japonicum

complementary DNA resource

Nat. Genet. 35 (2), 139-147 (2003)

12973349

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919 (ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

Location/Qualifiers

1..896

/organism="Schistosoma japonicum"

/mol_type="mRNA"

/db_xref="taxon:6182"

/sex="female"

/tissue_type="whole body"

/dev_stage="adult"

/lab_host="rabbits"

/clone_lib="SJF"

Query Match 4.3%; Score 20; DB 3; Length 896;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAAATAAATGGAACACACAT 22
|||||

Db 704 AAAATAAATGGAACACACAT 723
|||||

RESULT 15

BB212456/c

LOCUS BB212456

DEFINITION BB212456 RIKEN full-length enriched, 0 day neonate thymus Mus

musculus cDNA clone A430110009 3', mRNA sequence.

ACCESSION BB212456

VERSION BB212456.1 GI:8877409

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES source

Location/Qualifiers

1..679

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="T01000H3"

/db_xref="taxon:3712"

/clone="BOG092"

/clone_lib="BOGO"

/note="vector: pROS1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pROS1 using BstXI linkers"

Query Match 4.3%; Score 20; DB 11; Length 679;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 GGTATGATGTTTCTTC 345
|||||

Db 107 GGTATGATGTTTCTTC 88
|||||

RESULT 13

BZ162280/c

LOCUS BZ162280

DEFINITION BZ162280 TV CHORI-230 Segment 2 Rattus norvegicus genomic clone

CH230-276024, genomic survey sequence.

ACCESSION BZ162280

VERSION BZ162280.1 GI:23803252

KEYWORDS GSS.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 785)

AUTHORS Zhao, S., Shetty, J., Shatman, S., Tseng, G., Geer, K.,

Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,

Riggs, F., de Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 MboI segment

Unpublished (1999)

Other GSSs: CH230-276024.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Plate: 276 row: 0 column: 24

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..785

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/strain="BN/SnHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-276024"

/sex="female"

/cell_type="Brain"

/clone_lib="CHORI-230 Segment 2"

The Page Blank (uspo)
(oldsn) xuoq eeo si

GenCore version 5.1.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 21:32:07 ; Search time 97.5198 Seconds
(without alignments)
9311.708 Million cell updates/sec

Title: US-10-764-316-5
Perfect score: 468
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2461376 seqs, 970166171 residues

Word size : 1

Total number of hits satisfying chosen parameters: 4922276

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA New.*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	100.0	468	6	US-10-764-316-5
2	467	99.8	2305	6	US-10-764-316-3
3	300	64.1	412	8	US-11-136-524-10
C 4	19	4.1	1458	9	US-11-056-355B-72462
C 5	19	4.1	1461	9	US-11-056-355B-72470
C 6	18	3.8	575	8	US-11-266-748A-61868
C 7	18	3.8	691	6	US-10-953-349-3167
C 8	18	3.8	1000	8	US-11-266-748A-114823
C 9	18	3.8	1000	8	US-11-266-748A-119554
C 10	18	3.8	1000	8	US-11-266-748A-195502
C 11	18	3.8	1000	8	US-11-266-748A-281826
C 12	18	3.8	1000	8	US-11-266-748A-308466
C 13	18	3.8	1000	8	US-11-266-748A-390944
C 14	18	3.8	1000	8	US-11-266-748A-481662
C 15	18	3.8	1037	8	US-11-266-748A-931124
C 16	18	3.8	1037	8	US-11-266-748A-145935
C 17	18	3.8	1356	9	US-11-348-413-13626
C 18	18	3.8	1952	6	US-10-449-902-28210
C 19	18	3.8	5526	6	US-10-540-898-796
C 20	18	3.8	12610	6	US-10-517-441-441
C 21	18	3.8	12610	6	US-10-517-441-715
C 22	18	3.8	84675	6	US-10-539-228-398
C 23	18	3.8	109661	6	US-10-540-898-795

C 24	18	3.8	130877	6	US-10-539-228-54	Sequence 54, Appl
C 25	17	3.6	201	7	US-11-073-360-5989	Sequence 5989, Ap
C 26	17	3.6	484	8	US-11-266-748A-37795	Sequence 37795, A
C 27	17	3.6	558	8	US-11-266-748A-162781	Sequence 162781, A
C 28	17	3.6	570	8	US-11-266-748A-171938	Sequence 171938, A
C 29	17	3.6	570	8	US-11-266-748A-245466	Sequence 245466, A
C 30	17	3.6	598	6	US-10-513-369-3617	Sequence 3617, Ap
C 31	17	3.6	604	8	US-11-266-748A-299723	Sequence 299723, Ap
C 32	17	3.6	652	8	US-11-266-748A-11817	Sequence 11817, A
C 33	17	3.6	685	8	US-11-266-748A-480363	Sequence 480363, A
C 34	17	3.6	702	8	US-11-266-748A-191891	Sequence 191891, A
C 35	17	3.6	702	8	US-11-266-748A-226061	Sequence 226061, A
C 36	17	3.6	740	9	US-11-056-355B-56754	Sequence 56754, A
C 37	17	3.6	807	8	US-11-246-999-22	Sequence 22, Appl
C 38	17	3.6	846	8	US-11-266-748A-250972	Sequence 250972, A
C 39	17	3.6	846	8	US-11-266-748A-311489	Sequence 311489, A
C 40	17	3.6	950	8	US-11-266-748A-348672	Sequence 348672, A
C 41	17	3.6	950	8	US-11-266-748A-432051	Sequence 432051, A
C 42	17	3.6	1000	8	US-11-266-748A-198066	Sequence 198066, A
C 43	17	3.6	1000	8	US-11-266-748A-205770	Sequence 205770, A
C 44	17	3.6	1000	8	US-11-266-748A-286159	Sequence 286159, A
C 45	17	3.6	1000	8	US-11-266-748A-337588	Sequence 337588, A

ALIGNMENTS

RESULT 1

US-10-764-316-5
; Sequence 5, Application US/10764316
; Publication No. US20060127359A1
; GENERAL INFORMATION:
; APPLICANT: BORELLI, MICHAEL J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HEAT ACTIVATED GENE
; FILE REFERENCE: 10546-109
; CURRENT APPLICATION NUMBER: US/10764,316
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,473
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-764-316-5

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Best Local Similarity	100.0%;	Pred. No. 4.4e-254;		
Matches	468;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Qy	61	CCTGATGTTTCAGAGGACGAGGAGTACAGAGTCTTCTGCAACGTTGACTGAGCGAGAAAT	120	
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Qy	121	TAGCACTCTCGGTATTCCTCGATGAATGATATATCTTGGAAATACCGGAACCAATAGTCGCCC	180	
Db	121	TAGCACTCTCGGTATTCCTCGATGAATGATATATCTTGGAAATACCGGAACCAATAGTCGCCC	180	
Qy	181	ACAGGAGTGTGTTATATATATTTCTCACTGTTGATGATTCGCTAACAGAGTAAATCTTGC	240	
Db	181	ACAGGAGTGTGTTATATATATTTCTCACTGTTGATGATTCGCTAACAGAGTAAATCTTGC	240	
Qy	241	GATTGTTTCAACAGAGAGCTGATGAGGTGATTTGTTATACCTTCCCACTGTTGATC	300	
Db	241	GATTGTTTCAACAGAGAGCTGATGAGGTGATTTGTTATACCTTCCCACTGTTGATC	300	
Qy	301	ACGACCGATCATCGGCATTAGAATTGGAATGATGTTTCTTCTCAACCCATGATTCGC	360	

us-10-764-316-5-olig.rnpbn

Mon Nov 6 11:55:54 2006

```

; Publication No. US20060094034A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Josee
; APPLICANT: BEKEL, Sadjia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/11/136,524
; CURRENT FILING DATE: 2005-05-25
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-136-524-10

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Best Local Similarity 100.0%; Pred. No. 4.3e-159; Indels 0; Gaps 0;
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QY 169 CAATAGTCGCCACAGAGGTTGTTTATATATTTCTCACGTGTTGATGATCGTAAACAG 228
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QY 229 AGTAAATCTTGGGATTGTTTCAAAACAGAGAGCTGATGAGTGATTTATACCTCTCC 288
DB 61 AGTAAATCTTGGGATTGTTTCAAAACAGAGAGCTGATGAGTGATTTATACCTCTCC 120

QY 289 AACTGTTGATCACGACCGATCATCGGATTCGTAATAGAAATGTAATGATTTCTTCTCAAC 348
DB 121 AACTGTTGATCACGACCGATCATCGGATTCGTAATAGAAATGTAATGATTTCTTCTCAAC 180

QY 349 CCATGATTGGCGAATCGGGGCGTGGATTTCAGAGCAATTTGTAATAGTGTGTTTGGATT 408
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QY 409 CTTCAACAGACAAACGGAATCCTATAGACAGCGCGTAACTGATGATTCAGAGGATTT 468
DB 241 CTTCAACAGACAAACGGAATCCTATAGACAGCGCGTAACTGATGATTCAGAGGATTT 300

; Publication No. US20060127359A1
; GENERAL INFORMATION:
; APPLICANT: BORRELLI, MICHAEL J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HEAT ACTIVATED GENE
; FILE REFERENCE: 10546-109
; CURRENT APPLICATION NUMBER: US/10/764,316
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,473
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 2305
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-764-316-3

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Best Local Similarity 100.0%; Pred. No. 1.8e-253; Indels 0; Gaps 0;
Matches 467; Conservative 0; Mismatches 0;

QY 2 GAAATAAATGGAACACACATGTCGACACTGTTGACGGAAGTGTGCTGTGATATC 61
DB 1019 GAAATAAATGGAACACACATGTCGACACTGTTGACGGAAGTGTGCTGTGATATC 1078

QY 62 CTGATGTTTCAGAGCGGAGGCGAGTACAGCTTCTGCAAGCTTGAATGAGTAACTTTG 121
DB 1079 CTGATGTTTCAGAGCGGAGGCGAGTACAGCTTCTGCAAGCTTGAATGAGTAACTTTG 1138

QY 122 AGCACTCTCTGTTATTCGATGATGATGATGATGATGATGATGATGATGATGATG 181
DB 1139 AGCACTCTCTGTTATTCGATGATGATGATGATGATGATGATGATGATGATGATG 1198

QY 182 CAGGATGTTTATATATTTCTCAGCTGTTGATGATGATGATGATGATGATGATGATG 241
DB 1199 CAGGATGTTTATATATTTCTCAGCTGTTGATGATGATGATGATGATGATGATGATG 1258

QY 242 ATTGTTTCAACAGAGAGCTGATGAGTGTGATGATGATGATGATGATGATGATGATG 301
DB 1259 ATTGTTTCAACAGAGAGCTGATGAGTGTGATGATGATGATGATGATGATGATGATG 1318

QY 302 CGACCGATCATCGGCATTAAGATTTGGTAATGATGATGATGATGATGATGATGATG 361
DB 1319 CGACCGATCATCGGCATTAAGATTTGGTAATGATGATGATGATGATGATGATGATG 1378

QY 362 AATCGGCGGTGGATTCAGAGGCAATTTGTAATAGTGTGTTTCTTCAACAGACAA 421
DB 1379 AATCGGCGGTGGATTCAGAGGCAATTTGTAATAGTGTGTTTCTTCAACAGACAA 1438

QY 422 ACGGATCTTATAAGACAGCGCGCTAACTGGATGATTCAGAGGATTT 468
DB 1439 ACGGATCTTATAAGACAGCGCGCTAACTGGATGATTCAGAGGATTT 1485

; Publication No. US10764316
; Sequence 3, Application US/10764316
; Publication No. US20060127359A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Josee
; APPLICANT: BEKEL, Sadjia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/11/136,524
; CURRENT FILING DATE: 2005-05-25
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-136-524-10

Query Match      64.1%; Score 300; DB 8; Length 412;
Best Local Similarity 100.0%; Pred. No. 4.3e-159; Indels 0; Gaps 0;
Matches 300; Conservative 0; Mismatches 0;

QY 169 CAATAGTCGCCACAGAGGTTGTTTATATATTTCTCACGTGTTGATGATCGTAAACAG 228
DB 1 CAATAGTCGCCACAGAGGTTGTTTATATATTTCTCACGTGTTGATGATCGTAAACAG 60

QY 229 AGTAAATCTTGGGATTGTTTCAAAACAGAGAGCTGATGAGTGATTTATACCTCTCC 288
DB 61 AGTAAATCTTGGGATTGTTTCAAAACAGAGAGCTGATGAGTGATTTATACCTCTCC 120

QY 289 AACTGTTGATCACGACCGATCATCGGATTCGTAATAGAAATGTAATGATTTCTTCTCAAC 348
DB 121 AACTGTTGATCACGACCGATCATCGGATTCGTAATAGAAATGTAATGATTTCTTCTCAAC 180

QY 349 CCATGATTGGCGAATCGGGGCGTGGATTTCAGAGCAATTTGTAATAGTGTGTTTGGATT 408
DB 181 CCATGATTGGCGAATCGGGGCGTGGATTTCAGAGCAATTTGTAATAGTGTGTTTGGATT 240

QY 409 CTTCAACAGACAAACGGAATCCTATAGACAGCGCGTAACTGATGATTCAGAGGATTT 468
DB 241 CTTCAACAGACAAACGGAATCCTATAGACAGCGCGTAACTGATGATTCAGAGGATTT 300
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RESULT 4
US-11-056-355B-72462/C
; Sequence 72462, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 72462
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1458)
; OTHER INFORMATION: Ceres Seq. ID no. 4935487
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1458)
; OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13574398
; OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-72462

Query Match      4.1%; Score 19; DB 9; Length 1458;
; Sequence 10, Application US/11136524
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Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TTGTTTCAACAGAGAGC 261
Db 1281 TTGTTTCAACAGAGAGC 1263

RESULT 5
US-11-056-355B-72470/c
; Sequence 72470, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 72470
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1461)
; OTHER INFORMATION: Ceres Seq. ID no. 4935571
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1461)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13574398
; OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-72470

Query Match 4.1%; Score 19; DB 9; Length 1461;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TTGTTTCAACAGAGAGC 261
Db 1284 TTGTTTCAACAGAGAGC 1266

RESULT 6
US-11-266-748A-61868/c
; Sequence 61868, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 61868
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (438)..(438)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (441)..(441)
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
; LOCATION: (551)..(551)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: n is a, c, g, or t
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; OTHER INFORMATION: n is a, c, g, or t
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US-11-266-748A-61868

Query Match 3.8%; Score 18; DB 8; Length 575;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 TGATGTTTCTCTCAAC 348
Db 90 TGATGTTTCTCTCAAC 73

RESULT 7
US-10-953-349-3167/c
; Sequence 3167, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3167
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; OTHER INFORMATION:
US-10-953-349-3167

Query Match 3.8%; Score 18; DB 6; Length 691;
Best Local Similarity 100.0%; Pred. No. 12;
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us-10-764-316-5.olig.rnpbn

Mon Nov 6 11:55:54 2006

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GTTATATATTTCTCACG 207
Db 689 GTTATATATTTCTCACG 672

RESULT 8

US-11-266-748A-114823
; Sequence 114823, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114823
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-114823

Query Match 3.8%; Score 18; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 327 GTAATGATGTTTCTTCT 344
Db 870 GTAATGATGTTTCTTCT 887

RESULT 9

US-11-266-748A-119954/c
; Sequence 119954, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 119954
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-119954

Query Match 3.8%; Score 18; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 327 GTAATGATGTTTCTTCT 344
Db 131 GTAATGATGTTTCTTCT 114

RESULT 10

US-11-266-748A-195502
; Sequence 195502, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195502
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-195502

Query Match 3.8%; Score 18; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 327 GTAATGATGTTTCTTCT 344
Db 870 GTAATGATGTTTCTTCT 887

RESULT 11

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US-11-266-748A-281826
; Sequence 281826, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 281826
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-281826

Query Match      3.8%; Score 18; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      327 GTAATGATGTTTCTTCT 344
Db      870 GTAATGATGTTTCTTCT 887

RESULT 12
US-11-266-748A-308466/c
; Sequence 308466, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 308466
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-308466

Query Match      3.8%; Score 18; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      327 GTAATGATGTTTCTTCT 344
Db      131 GTAATGATGTTTCTTCT 114

RESULT 13
US-11-266-748A-390944
; Sequence 390944, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 390944
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-390944

Query Match      3.8%; Score 18; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      327 GTAATGATGTTTCTTCT 344
Db      870 GTAATGATGTTTCTTCT 887

RESULT 14
US-11-266-748A-481662/c
; Sequence 481662, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
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Query Match 3.8%; Score 18; DB 8; Length 1037;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 365 AGTTCTTCAACAGACAAA 382
Search completed: November 4, 2006, 01:19:20
Job time : 99.5198 secs

;; TITLE OF INVENTION: Methods of Using the Same
;; FILE REFERENCE: 55815-0102 (319189)
;; CURRENT APPLICATION NUMBER: US/11/266,748A
;; CURRENT FILING DATE: 2005-11-03
;; PRIOR APPLICATION NUMBER: EP 04105479.2
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105482.6
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105483.4
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105507.0
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105485.9
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105484.2
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: US 60/662,276
;; PRIOR FILING DATE: 2005-03-14
;; PRIOR APPLICATION NUMBER: US 60/700,293
;; PRIOR FILING DATE: 2005-07-18
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;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 481662
;; LENGTH: 1000
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
US-11-266-748A-481662
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 327 GTAATGATGTTTCTTCT 344
DB 131 GTAATGATGTTTCTTCT 114

RESULT 15
US-11-266-748A-93124
; Sequence 93124, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93124
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-93124

GenCore version 5.1.9
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DM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 21:28:41 ; Search time 122.65 Seconds
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	3.8	1356	3	US-09-134-001C-617
3	18	3.8	1356	3	US-09-710-279-2907
C 4	18	3.8	3069	3	US-09-710-279-4352
5	18	3.8	3206	3	US-09-710-279-4382
C 6	18	3.8	4249	3	US-09-710-279-4133
7	18	3.8	34047	3	US-09-949-016-13503
8	18	3.8	67581	3	US-09-949-016-14768
9	18	3.8	67643	3	US-09-949-016-14760
C 10	18	3.8	17838	3	US-09-949-016-17595
C 11	18	3.8	15617	3	US-09-949-016-16191
12	18	3.8	193303	3	US-09-497-855A-37
13	18	3.8	193303	3	US-09-497-855A-44
14	18	3.8	202111	3	US-09-949-016-13877
15	17	3.6	38	3	US-09-371-772B-11741
16	17	3.6	38	5	US-10-138-674B-14018
17	17	3.6	198	3	US-09-248-796A-13245
18	17	3.6	338	3	US-09-513-999C-33496
19	17	3.6	601	3	US-09-949-016-42562
20	17	3.6	601	3	US-09-949-016-42563
21	17	3.6	601	3	US-09-949-016-42564
C 22	17	3.6	601	3	US-09-949-016-140295
C 23	17	3.6	601	3	US-09-949-016-140296

C 24	17	3.6	601	3	US-09-949-016-140297	Sequence 140297,
25	17	3.6	601	3	US-09-949-016-160534	Sequence 160534,
26	17	3.6	601	3	US-09-949-016-160535	Sequence 160535,
27	17	3.6	601	3	US-09-949-016-189929	Sequence 189929,
C 28	17	3.6	609	3	US-09-328-111-609	Sequence 609, App
C 29	17	3.6	1164	3	US-09-248-796A-2935	Sequence 2935, App
C 30	17	3.6	1183	3	US-09-949-016-3675	Sequence 3675, App
C 31	17	3.6	1197	3	US-09-328-352-1131	Sequence 1131, App
C 32	17	3.6	1386	3	US-09-328-352-981	Sequence 981, App
33	17	3.6	1467	3	US-09-489-039A-1303	Sequence 1303, App
34	17	3.6	2212	3	US-09-917-254-24	Sequence 24, Appli
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C 41	17	3.6	5822	3	US-09-502-540-668	Sequence 668, App
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43	17	3.6	27284	3	US-09-949-016-15417	Sequence 15417, A
44	17	3.6	28720	3	US-09-341-587-7	Sequence 7, Appli
C 45	17	3.6	38343	3	US-09-949-016-15714	Sequence 15714, A

ALIGNMENTS

RESULT 1

US-09-328-352-597
; Sequence 597, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 597
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-597

Query Match 3.8%; Score 18; DB 3; Length 1017;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 CATTAGAAATGGTAATGA 333
DB 471 CATTAGAAATGGTAATGA 488

RESULT 2

US-09-134-001C-617
; Sequence 617, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 617
; LENGTH: 1356
; TYPE: DNA

Mon Nov 6 11:55:54 2006

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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-617

Query Match      3.8%; Score 18; DB 3; Length 1356;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 GATGATTGCAGGAGATT 468
Db 702 GATGATTGCAGGAGATT 719

RESULT 3
US-09-710-279-2907
; Sequence 2907, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2907
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-2907

Query Match      3.8%; Score 18; DB 3; Length 1356;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 GATGATTGCAGGAGATT 468
Db 702 GATGATTGCAGGAGATT 719

RESULT 4
US-09-710-279-4352/c
; Sequence 4352, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4352
; LENGTH: 3069
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4352

Query Match      3.8%; Score 18; DB 3; Length 3069;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 GATGATTGCAGGAGATT 468
Db 702 GATGATTGCAGGAGATT 468

RESULT 5
US-09-710-279-4382
; Sequence 4382, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4382
; LENGTH: 3206
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4382

Query Match      3.8%; Score 18; DB 3; Length 3206;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 GATGATTGCAGGAGATT 468
Db 2000 GATGATTGCAGGAGATT 2017

RESULT 6
US-09-710-279-4133/c
; Sequence 4133, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4133
; LENGTH: 4249
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4133

Query Match      3.8%; Score 18; DB 3; Length 4249;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 GATGATTGCAGGAGATT 468
Db 4145 GATGATTGCAGGAGATT 4128

RESULT 7
US-09-949-016-13503
; Sequence 13503, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```



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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13503
; LENGTH: 34047
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(34047)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13503

Query Match          3.8%; Score 18; DB 3; Length 34047;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      329 AATGATGTTTCTCTCA 346
        |||||
Db      20376 AATGATGTTTCTCTCA 20393

RESULT 8
US-09-949-016-14768
; Sequence 14768, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14768
; LENGTH: 67581
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(67581)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14768

Query Match          3.8%; Score 18; DB 3; Length 67581;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      321 GAATTGGTAATGATGTTT 338
        |||||
Db      10604 GAATTGGTAATGATGTTT 10621

RESULT 9
US-09-949-016-14760
; Sequence 14760, Application US/09949016
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14760
; LENGTH: 67643
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(67643)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14760

Query Match          3.8%; Score 18; DB 3; Length 67643;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      321 GAATTGGTAATGATGTTT 338
        |||||
Db      10592 GAATTGGTAATGATGTTT 10609
```

```
RESULT 10
US-09-949-016-17595/c
; Sequence 17595, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17595
; LENGTH: 117838
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(117838)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17595

Query Match          3.8%; Score 18; DB 3; Length 117838;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      405 AGTTCTTCAACAGACAAA 422
        |||||
Db      18984 AGTTCTTCAACAGACAAA 18967
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us-10-764-316-5.011g.rn1

Mon Nov 6 11:55:54 2006

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RESULT 11
US-09-949-016-16191/c
; Sequence 16191, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16191
; LENGTH: 155617
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16191

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Query Match          3.8%; Score 18; DB 3; Length 155617;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 183 AGGAGTGTGTATATT 200
Db 108176 AGGAGTGTGTATATT 108159

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RESULT 12
US-09-497-855A-37
; Sequence 37, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 193303
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-37

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Query Match          3.8%; Score 18; DB 3; Length 193303;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 331 TGATGTTTCTCTCAAC 348
Db 161051 TGATGTTTCTCTCAAC 161068

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RESULT 13
US-09-497-855A-44
; Sequence 44, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523

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```

; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 193303
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-44

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Query Match          3.8%; Score 18; DB 3; Length 193303;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 331 TGATGTTTCTCTCAAC 348
Db 161051 TGATGTTTCTCTCAAC 161068

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RESULT 14
US-09-949-016-13877
; Sequence 13877, Application US/09949016
; Patent No. 8812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13877
; LENGTH: 202111
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(202111)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13877

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Query Match          3.8%; Score 18; DB 3; Length 202111;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 185 GAGTTGTTTATATATTC 202
Db 74832 GAGTTGTTTATATATTC 74849

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RESULT 15
US-09-371-772B-11741
; Sequence 11741, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Favco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: Levels of Vascular Endothelial Growth Factor Receptor

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; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11741
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-11741

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Query Match      3.6%; Score 17; DB 3; Length 38;
Best Local Similarity 88.2%; Pred. No. 73;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      253 CAGAAGAGCTGATGAGG 269
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Db       1 CAGAAGAGCTGATGAGG 17

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OM nucleic - nucleic search, using sw model

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	4.3	83710	9	US-10-417-375-27
3	19	4.1	496	4	US-09-925-065A-426352
4	19	4.1	496	5	US-09-925-065A-426352
5	19	4.1	497	12	US-10-301-480-489880
6	19	4.1	497	12	US-10-301-480-1103289
7	19	4.1	506	12	US-10-301-480-59270
8	19	4.1	506	12	US-10-301-480-59271
9	19	4.1	506	12	US-10-301-480-59272
10	19	4.1	506	12	US-10-301-480-672679
11	19	4.1	506	12	US-10-301-480-672680
12	19	4.1	506	12	US-10-301-480-672681
13	19	4.1	520	6	US-10-027-632-208513
14	19	4.1	520	6	US-10-027-632-208514
15	19	4.1	520	6	US-10-027-632-208515
16	19	4.1	520	7	US-10-027-632-208513
17	19	4.1	520	7	US-10-027-632-208514

Sequence 208515,	7	US-10-027-632-208515	520	4.1	19	4.1
Sequence 489881,	12	US-10-301-480-489881	615	4.1	19	4.1
Sequence 1103290,	12	US-10-301-480-1103290	615	4.1	19	4.1
Sequence 29902, A	16	US-11-096-568A-29902	1458	4.1	19	4.1
Sequence 29906, A	16	US-11-096-568A-29906	1461	4.1	19	4.1
Sequence 379, App	3	US-09-764-878-379	32189	4.1	19	4.1
Sequence 379, App	6	US-10-079-854-379	32189	4.1	19	4.1
Sequence 377, App	3	US-09-764-878-377	32221	4.1	19	4.1
Sequence 377, App	6	US-10-079-854-377	32221	4.1	19	4.1
Sequence 450106,	8	US-10-719-956-450106	25	3.8	18	3.8
Sequence 226608,	9	US-10-719-900-226608	25	3.8	18	3.8
Sequence 324160,	16	US-11-136-527-324160	25	3.8	18	3.8
Sequence 3985, Ap	3	US-09-864-408A-3985	278	3.8	18	3.8
Sequence 53166, A	12	US-10-301-480-53166	423	3.8	18	3.8
Sequence 666575,	12	US-10-301-480-666575	423	3.8	18	3.8
Sequence 46151, A	9	US-10-357-930-46151	455	3.8	18	3.8
Sequence 199207,	6	US-10-027-632-199207	474	3.8	18	3.8
Sequence 199207,	7	US-10-027-632-199207	474	3.8	18	3.8
Sequence 174541,	6	US-10-027-632-174541	481	3.8	18	3.8
Sequence 174542,	6	US-10-027-632-174542	481	3.8	18	3.8
Sequence 298848,	6	US-10-027-632-298848	481	3.8	18	3.8
Sequence 298849,	6	US-10-027-632-298849	481	3.8	18	3.8
Sequence 174541,	7	US-10-027-632-174541	481	3.8	18	3.8
Sequence 174542,	7	US-10-027-632-174542	481	3.8	18	3.8
Sequence 298848,	7	US-10-027-632-298848	481	3.8	18	3.8
Sequence 298849,	7	US-10-027-632-298849	481	3.8	18	3.8
Sequence 220154,	4	US-09-925-065A-220154	503	3.8	18	3.8
Sequence 220154,	5	US-09-925-065A-220154	503	3.8	18	3.8

ALIGNMENTS

RESULT 1

US-10-425-821-10

; Sequence 10, Application US/10425821

; Publication No. US20040219530A1

; GENERAL INFORMATION:

; APPLICANT: BROUSSEAU, Roland

; APPLICANT: HAREL, Jos e

; APPLICANT: BEKAL, Sadjia

; TITLE OF INVENTION: ARRAY AND USBS THEREOF

; FILE REFERENCE: 86369-3

; CURRENT APPLICATION NUMBER: US/10/425,821

; CURRENT FILING DATE: 2003-04-30

; NUMBER OF SEQ ID NOS: 176

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 412

; TYPE: DNA

; ORGANISM: Escherichia coli

US-10-425-821-10

Query Match 64.1%; Score 300; DB 9; Length 412;
Best Local Similarity 100.0%; Pred. No. 7.3e-156;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	169	CAATAGTCGCCACACAGGAGCTGTTATATATATTTCTCACGTTGATGCTTGCCTAACAG	228
Db	1	CAATAGTCGCCACACAGGAGCTGTTATATATTTCTCACGTTGATGCTTGCCTAACAG	60
Qy	229	AGTAAATCTTGGCATTTGTTTCAACAGAGAGCTGATGAGGTGATGTTATTTACCTCTCC	288
Db	61	AGTAAATCTTGGCATTTGTTTCAACAGAGAGCTGATGAGGTGATGTTATTTACCTCTCC	120
Qy	289	AACTGTTGATCAGCCGATCATCGGCAATTAAGATTGTAATGATGTTTCTTCTCAAC	348
Db	121	AACTGTTGATCAGCCGATCATCGGCAATTAAGATTGTAATGATGTTTCTTCTCAAC	180
Qy	349	CAATGATTTGGCAATCGGGCGTGGATTCAGGAGCAATTTGTAATGATGTTTCTTCTCAAC	408
Db	181	CAATGATTTGGCAATCGGGCGTGGATTCAGGAGCAATTTGTAATGATGTTTCTTCTCAAC	240

us-10-764-316-5.olig.rnpbm

Mon Nov 6 11:55:54 2006

QY 409 CTTCAACAGACAAACGGATCCTATAAGACAGCGCGCTAACTGGATGATTCACGAGATTT 468
Db 241 CTTCAACAGACAAACGGATCCTATAAGACAGCGCGCTAACTGGATGATTCACGAGATTT 300

RESULT 2
US-10-417-375-27/c
; Sequence 27, Application US/10417375
; Publication No. US20040219528A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 83710
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(83710)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375-27

Query Match 4.3%; Score 20; DB 9; Length 83710;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ATTAGCACTCTCGGTATTC 137
Db 3171 ATTAGCACTCTCGGTATTC 3152

RESULT 3
US-09-925-065A-426352
; Sequence 426352, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426352
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-426352

Query Match 4.1%; Score 19; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 GGTAAATGATGTTTCTTCT 344
Db 158 GGTAAATGATGTTTCTTCT 176

RESULT 4
US-09-925-065A-426352
; Sequence 426352, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426352
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-426352

Query Match 4.1%; Score 19; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 GGTAAATGATGTTTCTTCT 344
Db 158 GGTAAATGATGTTTCTTCT 176

RESULT 5
US-10-301-480-489880
; Sequence 489880, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1228818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 489880
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-489880

Query Match 4.1%; Score 19; DB 12; Length 497;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 GGTAAATGATGTTTCTTCT 344
Db 158 GGTAAATGATGTTTCTTCT 176

RESULT 6

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US-10-301-480-1103289
; Sequence 1103289, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1103289
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1103289

Query Match
Best Local Similarity 4.1%; Score 19; DB 12; Length 497;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 GGTAATGATGTTTCTTCT 344
Db 158 GGTAATGATGTTTCTTCT 176

RESULT 7
US-10-301-480-59270/c
; Sequence 59270, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59270
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-59270

Query Match
Best Local Similarity 4.1%; Score 19; DB 12; Length 506;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 CTGATGTTTCAGGAGCAG 80
Db 241 CTGATGTTTCAGGAGCAG 223

RESULT 8
US-10-301-480-59271/c
; Sequence 59271, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
```

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; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59271
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-59271

Query Match
Best Local Similarity 4.1%; Score 19; DB 12; Length 506;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 CTGATGTTTCAGGAGCAG 80
Db 241 CTGATGTTTCAGGAGCAG 223

RESULT 9
US-10-301-480-59272/c
; Sequence 59272, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59272
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-59272

Query Match
Best Local Similarity 4.1%; Score 19; DB 12; Length 506;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 CTGATGTTTCAGGAGCAG 80
Db 241 CTGATGTTTCAGGAGCAG 223

RESULT 10
US-10-301-480-672679/c
; Sequence 672679, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 672679
; LENGTH: 506
```

us-10-764-316-5.olig.rnpbm

Mon Nov 6 11:55:54 2006

```

; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-672679

Query Match      4.1%; Score 19; DB 12; Length 506;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      62 CTGATGGTTCAGGAGGCAG 80
DB      241 CTGATGGTTCAGGAGGCAG 223

RESULT 11
US-10-301-480-672680/c
; Sequence 672680, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672680
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-672680

```

```

Query Match      4.1%; Score 19; DB 12; Length 506;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      62 CTGATGGTTCAGGAGGCAG 80
DB      241 CTGATGGTTCAGGAGGCAG 223

RESULT 12
US-10-301-480-672681/c
; Sequence 672681, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672681
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-672681

Query Match      4.1%; Score 19; DB 12; Length 506;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      62 CTGATGGTTCAGGAGGCAG 80

```

```

DB      241 CTGATGGTTCAGGAGGCAG 223

RESULT 13
US-10-027-632-208513/c
; Sequence 208513, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208513
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-208513

Query Match      4.1%; Score 19; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      62 CTGATGGTTCAGGAGGCAG 80
DB      240 CTGATGGTTCAGGAGGCAG 222

RESULT 14
US-10-027-632-208514/c
; Sequence 208514, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

```



```
; SEQ ID NO 208514
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-208514
```

```
Query Match      4.1%; Score 19; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      62 CTGATGGTTCAGGAGGCAG 80
Db      240 CTGATGGTTCAGGAGGCAG 222
```

```
RESULT 15
US-10-027-632-208515/c
; Sequence 208515, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208515
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-208515
```

```
Query Match      4.1%; Score 19; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      62 CTGATGGTTCAGGAGGCAG 80
Db      240 CTGATGGTTCAGGAGGCAG 222
```

```
Search completed: November 3, 2006, 23:12:50
Job time : 636.59 secs
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Green Bank (USGS)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 20:16:55 ; Search time 273.593 Seconds
(without alignments)
11926.532 Million cell updates/sec

Title: US-10-764-316-5
Perfect score: 468
Sequence: 1 tgaataataatgaacacac.....tggatgattgcaggagattt 468

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1
Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	64.1	412	13	Adt98253 E. coli c
2	44	9.4	822	4	Aaf85771 E coli cy
3	20	4.3	8102	13	Abd32667 Mouse can
4	19	4.1	32189	5	Aas30115 Human lun
5	19	4.1	32189	10	Adb33452 Human nov
6	19	4.1	32221	5	Aas30113 Human lun
7	19	4.1	32221	10	Adb33450 Human nov
8	18	3.8	278	6	Abn77046 Human ORF
9	18	3.8	309	10	Adl24711 Intestina
10	18	3.8	459	13	Acf85026 Human SIR
11	18	3.8	465	5	Abv46132 Human pro
12	18	3.8	565	3	Aac35341 Arabidops
13	18	3.8	565	15	Aef29701 Lead Cere
14	18	3.8	575	4	Aah12181 Human-CDN
15	18	3.8	675	3	Aaa70256 Plasmodiu
16	18	3.8	758	4	Aah04264 Human CDN
17	18	3.8	826	4	Abli4609 Drosophil
18	18	3.8	1017	9	Ada29310 DNA encod

ALIGNMENTS

RESULT 1

ID ADT98253 standard; DNA; 412 BP.

XX ADT98253;

XX AC ADT98253;

XX DT 27-JAN-2005 (first entry)

XX DE E. coli cdt1 DNA.

XX ds; array; pathotype; microorganism detection; infection; probe;
 KW virulence gene; enterotoxigenic E. coli; ETEC; enteropathogenic E. coli;
 KW EPEC; enterohemorrhagic E. coli; EHEC; enteroaggregative E. coli; EAEC;
 KW enteroinvasive E. coli; EIEC; uropathogenic strain; UPEC;
 KW neonatal meningitis; MENEC; septicemia; SEPEC; cell-detaching E. coli;
 KW CDEC; diffusely adherent E. coli; DAEC; toxin; adhesion factor;
 KW flagellar antigen; invasins; autotransporter protein;
 KW aerobactin system protein; food; water; air; soil; blood;
 KW urine; amniotic fluid; feces; diagnosis; diarrhea; hemorrhagic colitis;
 KW hemolytic uremic syndrome; invasive intestinal infection; dysentery;
 KW urinary tract infection; neonatal meningitis; septicemia; cdt1.

XX Escherichia coli.

OS US2004219530-A1.

XX PN 04-NOV-2004.

XX PD 30-APR-2003; 2003US-00425821.

XX PF 30-APR-2003; 2003US-00425821.

XX PR (BROU/) BROUSSEAU R.

XX PA (HARE/) HAREL J.

XX PA (BEKA/) BEKAL S.

XX PI Brousseau R, Harel J, Bekal S;

XX DR WPI; 2004-774932/76.

XX

Aah53757 S. epider
 Abn91154 Staphyloc
 Adt98253 Staphyloc
 Aak84295 Human imm
 Aah16394 Human CDN
 Aah15964 Human CDN
 Abli4608 Drosophil
 Adt97926 Full leng
 Aah54988 S. epider
 Aah5018 S. epider
 Aah54769 S. epider
 Adt97819 Human can
 Aah52637 Human che
 Aak65263 Human imm
 Adt98659 Oligonucl
 Adt989425 Oligonucl
 Aak65264 Human imm
 Aak65265 Human imm
 Aah9226 Escherich
 Aai99368 Human exc
 Aai63718 Human kid
 Abs79015 E. coli C
 Adh80582 Escherich
 Abd33325 Human can
 Adt97818 Human can
 Abd33104 Human can

19 18 1356 4 AAH53757
 20 18 1356 6 ABN91154
 21 18 1356 13 ADS02625
 22 18 1409 4 AAK84295
 23 18 1410 4 AAK84294
 24 18 1944 4 AAH16394
 25 18 2868 4 AAH15964
 26 18 2890 4 ABLI4608
 27 18 3008 13 ADT97926
 28 18 3069 4 AAH54988
 29 18 3206 4 AAH5018
 30 18 4249 4 AAH54769
 31 18 5526 12 ADT97819
 32 18 7434 6 AAD28387
 33 18 10324 4 AAK65263
 34 18 12610 13 ADS89659
 35 18 12610 13 ADS89425
 36 18 14136 4 AAK65264
 37 18 14387 4 AAK65265
 38 18 27324 4 ABA89226
 39 18 32249 4 AAI99368
 40 18 32249 5 AAI63718
 41 18 65011 6 ABS79015
 42 18 68611 10 ADH80582
 43 18 84675 13 ABD33325
 44 18 109661 12 ADT97818
 45 18 130877 13 ABD33104

RESULT 3
ABD32667/c
ID ABD32667 standard; DNA; 83102 BP.
AC
XX ABD32667;
XX
DT 18-NOV-2004 (first entry)
XX
DE Mouse cancer-associated genomic DNA MD13-073.
XX
KW Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
KW leukaemia; lymphoma; CAP.
OS Mus musculus.
XX
XX WO2004074320-A2.
XX
XX 02-SEP-2004.
XX
XX 17-FEB-2004; 2004WO-US004730.
XX
XX 14-FEB-2003; 2003US-00367094.
XX
XX 14-MAR-2003; 2003US-00388838.
XX
XX 15-APR-2003; 2003US-00417375.
XX
XX 13-JUN-2003; 2003US-00461862.
XX
XX 15-SEP-2003; 2003US-00663431.
XX
XX 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Morris DW, Malandro MS;
XX
XX WPI, 2004-652914/63.
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
XX disclosure; seqid 212; 310pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 83102 BP; 23417 A; 17147 C; 17240 G; 24360 T; 0 U; 938 Other;
Query Match 4.3%; Score 20; DB 13; Length 83102;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 118 ATTAGCACTCCTGGTATTC 137
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DB 3009 ATTAGCACTCCTGGTATTC 2990
RESULT 4
AAS30115
ID AAS30115 standard; DNA; 32189 BP.
XX
XX AAS30115;
AC
XX
XX 21-NOV-2001 (first entry)
DT
XX
XX Human lung antigen genomic DNA #185.
XX
XX Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW antineumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-infertility; food additive.
XX
XX Homo sapiens.
OS
XX WO200155303-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001301.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX
XX 04-FEB-2000; 2000US-0180628P.
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XX 24-FEB-2000; 2000US-0184664P.
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XX 02-MAR-2000; 2000US-0186350P.
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XX 16-MAR-2000; 2000US-0189874P.
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XX 17-MAR-2000; 2000US-0190076P.
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XX 18-APR-2000; 2000US-0198123P.
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XX 19-MAY-2000; 2000US-0205515P.
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XX 07-JUN-2000; 2000US-0209467P.
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XX 28-JUN-2000; 2000US-0214886P.
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XX 30-JUN-2000; 2000US-0215135P.
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XX 11-JUL-2000; 2000US-0217487P.
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XX 14-JUL-2000; 2000US-0218290P.
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XX 26-JUL-2000; 2000US-0220963P.
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XX 26-JUL-2000; 2000US-0220964P.
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XX 14-AUG-2000; 2000US-0224518P.
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XX 14-AUG-2000; 2000US-0224519P.
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XX 14-AUG-2000; 2000US-0225214P.
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XX 14-AUG-2000; 2000US-0225266P.
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XX 14-AUG-2000; 2000US-0225267P.
XX
XX 14-AUG-2000; 2000US-0225268P.
XX
XX 14-AUG-2000; 2000US-0225270P.
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XX 14-AUG-2000; 2000US-0225447P.
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XX 18-AUG-2000; 2000US-0225759P.
XX
XX 22-AUG-2000; 2000US-0226279P.
XX
XX 22-AUG-2000; 2000US-0226681P.

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PR	22-AUG-2000;	2000US-0226868P.	PR	17-NOV-2000;	2000US-0249208P.
PR	22-AUG-2000;	2000US-0227182P.	PR	17-NOV-2000;	2000US-0249209P.
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PR	06-SEP-2000;	2000US-0230437P.	PR	17-NOV-2000;	2000US-0249218P.
PR	06-SEP-2000;	2000US-0230438P.	PR	17-NOV-2000;	2000US-0249244P.
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PR	14-SEP-2000;	2000US-0232398P.	PR	05-DEC-2000;	2000US-0251030P.
PR	14-SEP-2000;	2000US-0232399P.	PR	05-DEC-2000;	2000US-0251988P.
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PR	21-SEP-2000;	2000US-0234274P.	PR	08-DEC-2000;	2000US-0251990P.
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PR	26-SEP-2000;	2000US-0235484P.	XX	(HUMA-) HUMAN GENOME SCI INC.	
PR	27-SEP-2000;	2000US-0235834P.	XX	Rosen CA, Barash SC, Ruben SM;	
PR	27-SEP-2000;	2000US-0235836P.	PI	WPI; 2001-457723/49.	
PR	29-SEP-2000;	2000US-0236327P.	DR		
PR	29-SEP-2000;	2000US-0236367P.	XX		
PR	29-SEP-2000;	2000US-0236368P.	XX		
PR	29-SEP-2000;	2000US-0236369P.	PT		
PR	29-SEP-2000;	2000US-0236370P.	PT		
PR	02-OCT-2000;	2000US-0236802P.	XX		
PR	02-OCT-2000;	2000US-0237037P.	PS	Claim 1; SEQ ID NO 379; 507pp; English.	
PR	02-OCT-2000;	2000US-0237038P.	XX		
PR	02-OCT-2000;	2000US-0237039P.	CC	Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode	
PR	02-OCT-2000;	2000US-0237040P.	CC	the lung antigen polypeptides of the invention. lung antigen polypeptides	
PR	13-OCT-2000;	2000US-0239935P.	CC	and their associated polynucleotides are useful in the diagnosis,	
PR	20-OCT-2000;	2000US-0240960P.	CC	treatment and prevention of various types of disorders in e.g. humans,	
PR	20-OCT-2000;	2000US-0241221P.	CC	mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A	
PR	20-OCT-2000;	2000US-0241785P.	CC	pathological condition can be determined by detecting the presence or	
PR	20-OCT-2000;	2000US-0241786P.	CC	absence of a mutation in a lung antigen polynucleotide. The treatable	
PR	20-OCT-2000;	2000US-0241787P.	CC	disorders include autoimmune diseases such as rheumatoid arthritis,	
PR	20-OCT-2000;	2000US-0241808P.	CC	hyperproliferative disorders such as cardiac arrest, cerebrovascular	
PR	20-OCT-2000;	2000US-0241809P.	CC	disorders such as cerebral ischaemia, nervous system disorders such as	
PR	01-NOV-2000;	2000US-0244617P.	CC	Alzheimer's disease. Infections caused by bacteria, viruses and fungi,	
PR	08-NOV-2000;	2000US-0246474P.	CC	ocular disorders such as corneal infection, gastrointestinal disorders such as	
PR	08-NOV-2000;	2000US-0246475P.	CC	premature labour and infertility, gastroscoliosis and	
PR	08-NOV-2000;	2000US-0246476P.	CC	Crohn's disease, renal disorders such as asthma and pleurisy. The polypeptides can	
PR	08-NOV-2000;	2000US-0246477P.	CC	also be used to aid wound healing, to prevent skin aging due to sunburn,	
PR	08-NOV-2000;	2000US-0246478P.	CC	to maintain organs before transplantation, to regenerate tissues and in	
PR	08-NOV-2000;	2000US-0246523P.	CC	chemotaxis. The polypeptides can also be used as a food additive or	
PR	08-NOV-2000;	2000US-0246524P.	CC	preservative to increase or decrease storage capabilities. Note: The	
PR	08-NOV-2000;	2000US-0246525P.	CC	sequence data for this patent did not form part of the printed	
PR	08-NOV-2000;	2000US-0246526P.	CC	specification, but was obtained in electronic format directly from WIPO	
PR	08-NOV-2000;	2000US-0246527P.	CC	at ftp.wipo.int/pub/published_pct_sequences	
PR	08-NOV-2000;	2000US-0246528P.			
PR	08-NOV-2000;	2000US-0246532P.			
PR	08-NOV-2000;	2000US-0246609P.			
PR	08-NOV-2000;	2000US-0246610P.			
PR	08-NOV-2000;	2000US-0246611P.			
PR	08-NOV-2000;	2000US-0246613P.			
PR	17-NOV-2000;	2000US-0249207P.			
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			Best Local Similarity 100.0%; Pred. No. 26;		
			Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
			62 CTGATGGTTCAGGAGCAG 80		
			QY		

Db 23959 CTGATGTTCCAGGAGCAG 23977
RESULT 5
ADB33452
ID ADB33452 standard; DNA, 32189 BP.
XX AC ADB33452;
XX DT 04-DEC-2003 (first entry)
XX DE Human novel lung related polypeptide DNA SEQ ID NO 379.
XX gene therapy; lung antigen; neoplasia; acute myelogenous leukaemia;
XX adenocarcinoma; respiratory disorder; chronic rhinitis; sinusitis;
XX immunodeficiency; X-linked agammaglobulinemia;
XX X-linked infantile agammaglobulinemia; inflammatory disorder;
XX adrenailitis; alveolitis; immune complex disease; serum sickness;
XX polyarteritis nodosa; bleeding disorder; thrombocytopenia;
XX Von Willebrand's disease; acquired platelet dysfunction; kidney failure;
XX multiple myeloma; macrophage related disorder; Gaucher's disease;
XX Niemann-pick disease; tumour; colon cancer; pancreatic cancer;
XX renal disorder; nephritis; bone disorder; Albers-Schonberg disease;
XX bowleg; muscle disorder; Becker's muscular dystrophy;
XX Duchenne's muscular dystrophy; nervous disorder; ischaemic lesion;
XX traumatic lesion; endocrine disorder; Cushing's syndrome;
XX corticosteroid deficiency; gastrointestinal disorder; dysphagia;
XX gastric reflux; human; ds.
XX OS Homo sapiens.
XX PN US2003054368-A1.
XX PD 20-MAR-2003.
XX PF 22-FEB-2002; 2002US-00079854.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 14-AUG-2000; 2000US-0225758P.
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PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
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PR 22-AUG-2000; 2000US-0227182P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
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PR 02-OCT-2000; 2000US-0237040P.
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PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
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PR 17-NOV-2000; 2000US-0249207P.
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PR	05-DEC-2000;	2000US-0256719P.	
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PR	08-DEC-2000;	2000US-0251856P.	
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PR	08-DEC-2000;	2000US-0251869P.	
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PR	11-DEC-2000;	2000US-0254097P.	
PR	05-JAN-2001;	2001US-0259678P.	
PR	17-JAN-2001;	2001US-00764878.	
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA			
XX	Rosen CA, Ruben SM, Barash SC;		
PI			
XX	WPI; 2003-695900/66.		
DR			
XX	Novel isolated lung antigen polypeptides useful for treating, preventing,		
PT	diagnosing acute myelogenous leukemias, adenocarcinoma, thrombocytopenia,		
PT	Von Willebrand's disease.		
PT			
XX	Disclosure; SEQ ID NO 379; 178pp; English.		
PS			
XX	The invention relates to an isolated lung antigen polypeptide sequence or		
CC	encoded sequence in a cDNA clone. The polypeptide and its polynucleotide		
CC	are useful for treating, preventing, diagnosing and/or prognosing		
CC	diseases and/or disorders such as pathological cell proliferative		
CC	neoplasias e.g. acute myelogenous leukemias, adenocarcinoma; respiratory		
CC	disorders such as chronic rhinitis, sinusitis; immunodeficiencies such as		
CC	X-linked agammaglobulinemia, X-linked infantile agammaglobulinaemia;		
CC	inflammatory disorders such as adenitis, alveolitis; immune complex		
CC	diseases such as serum sickness, polyarteritis nodosa; bleeding disorders		
CC	such as thrombocytopenia, Von Willebrand's disease; acquired platelet		
CC	dysfunction such as kidney failure, multiple myeloma; disorders		
CC	associated with macrophage numbers and/or macrophage function such as		
CC	Gaucher's disease, Niemann-Pick disease; tumours such as colon cancer,		
CC	pancreatic cancer, renal disorders such as kidney failure, nephritis;		
CC	bone disorders such as Albers-Schonberg disease, bowlegs; muscle		
CC	disorders such as Becker's muscular dystrophy, Duchenne's muscular		
CC	dystrophy; nervous disorders such as ischaemic lesions, traumatic lesions		
CC	; endocrine disorders such as Cushing's syndrome, corticosteroid		
Query Match	4.1%; Score 19; DB 10; Length 32189;		
Best Local Similarity	100.0%; Pred. No. 26;		
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	62 CTGATGCTTCAGGAGGCAG 80		
Db	23959 CTGATGCTTCAGGAGGCAG 23977		
RESULT 6			
AAS30113			
ID	AAS30113 standard; DNA; 32221 BP.		


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PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232337P.
PR 14-SEP-2000; 2000US-0232398P.
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PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234988P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241321P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.

PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2000US-0254097P.
PR 05-JAN-2001; 2000US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-457723/49.
DR
XX
XX Isolated polypeptide for treating, preventing and/ or prognosing
PT respiratory disorders related to the lung including lung cancers and also
PT for testing and detection e.g. diagnosis.
XX
XX Claim 1; SEQ ID NO 377; 507pp; English.
XX
CC Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode
CC the lung antigen polypeptides of the invention. Lung antigen polypeptides
CC and their associated polynucleotides are useful in the diagnosis,
CC treatment and prevention of various types of disorders in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by detecting the presence or
CC absence of a mutation in a lung antigen polynucleotide. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischaemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma and pleurisy. The polypeptides can
CC also be used to aid wound healing, to prevent skin aging due to sunburn,
CC to maintain organs before transplantation, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 4.1%; Score 19; DB 5; Length 32221;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CTGATGGTTTCAGGAGGCAG 80
DB 23989 CTGATGGTTTCAGGAGGCAG 24007

RESULT 7
ADB33450
ID ADB33450 standard; DNA; 32221 BP.
XX
AC ADB33450;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human novel lung related polypeptide DNA SEQ ID NO 377.
XX
```


PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251398P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764878.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-695900/66.
XX Novel isolated lung antigen polypeptides useful for treating, preventing,
PT diagnosing acute myelogenous leukemias, adenocarcinoma, thrombocytopenia,
PT Von Willebrand's disease.
XX Disclosure; SEQ ID NO 377; 178pp; English.
XX The invention relates to an isolated lung antigen polypeptide sequence or
CC encoded sequence in a cDNA clone. The polypeptide and its polynucleotide
CC are useful for treating, preventing, diagnosing and/or prognosing
CC diseases and/or disorders such as pathological cell proliferative
CC neoplasias e.g. acute myelogenous leukemias, adenocarcinoma; respiratory
CC disorders such as chronic rhinitis, sinusitis; immunodeficiencies such as
CC X-linked agammaglobulinemia, X-linked infantile agammaglobulinemia;
CC inflammatory disorders such as adenitis, alveolitis; immune complex
CC diseases such as serum sickness, polyarteritis nodosa; bleeding disorders
CC such as thrombocytopenia, Von Willebrand's disease; acquired platelet
CC dysfunction such as kidney failure, multiple myeloma; disorders
CC associated with macrophage numbers and/or macrophage function such as
CC Gaucher's disease, Niemann-Pick disease; tumours such as colon cancer,
CC pancreatic cancer, renal disorders such as kidney failure, nephritis;
CC bone disorders such as Albers-Schonberg disease, bowlegs; muscle
CC disorders such as Becker's muscular dystrophy, Duchenne's muscular
CC dystrophy; nervous disorders such as ischaemic lesions, traumatic lesions
CC ; endocrine disorders such as Cushing's syndrome, corticosteroid

Query Match 4.1%; Score 19; DB 10; Length 32221;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CTGATGTTTCAGGAGGCG 80
Db 23989 CTGATGTTTCAGGAGGCG 24007

RESULT 8
ID ABN77046/C
XX ABN77046 standard; cDNA; 278 BP.
AC ABN77046;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human ORF1993 cDNA, SEQ ID NO:3985.
XX
KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristics; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;

KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulvovaginitis;
KW vasotrophic; antipsoriatic; antidiabetic; cytostatic; neutropenic;
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
XX Homo sapiens.
XX WO200190366-A2.
XX 29-NOV-2001.
XX 24-MAY-2001; 2001WO-US017076.
XX 24-MAY-2000; 2000US-0206690P.
XX (CURA-) CURAGEN CORP.
XX Leach MD, Shinkets RA;
XX WPI; 2002-106200/14.
XX P-PSDB; ABP33020.
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
PT transplantation.
XX Claim 1; Page 1253; 2508pp; English.
XX Sequences ABP31028-ABP3561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN7587 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC and antiinfective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases
XX
SQ Sequence 278 BP; 73 A; 74 C; 79 G; 52 T; 0 U; 0 Other;
Query Match 3.8%; Score 18; DB 6; Length 278;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 GCAGTACCAGCTTCGCA 100

PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142330P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142930P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144844P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145115P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-01455913P.
PR 27-JUL-1999; 99US-01455918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
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PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.

PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 08-OCT-1999; 99US-0158369P.
PR 12-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160880P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 3.8%; Score 18; DB 3; Length 565;
Best Local Similarity 100.0%; Pred.No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 397 TGTGTTTGAGTCTCTCAA 414
|||||
Db 57 TGTGTTTGAGTCTCTCAA 40

RESULT 13
AEF29701/c
ID AEF29701 standard; cDNA; 565 BP.
XX
AC AEF29701;
XX
DT 23-MAR-2006 (first entry)
XX
DE Lead_CeresClone cDNA SEQ ID NO:1901.
XX
KW ss; gene; plant; transgenic plant; crop improvement;
XX abiotic stress tolerance; plant growth regulation.
XX Arabidopsis thaliana.
XX
XX WO2006004955-A2.
XX
PD 12-JAN-2006.
XX
XX 30-JUN-2005; 2005WO-US023326.
XX
XX 30-JUN-2004; 2004US-0583621P.
XX 30-JUN-2004; 2004US-0584800P.
XX 30-JUN-2004; 2004US-0584829P.

XX PA (CERE-) CERES INC.
XX PI Alexandrov N, Brover V, Mascia P, Feldmann K;
XX DR WPI; 2006-090599/09.
XX DR P-FSDB; AEF29702.
XX
XX New isolated nucleic acid molecule modifying plant phenotypes and
XX PT characteristics and the polypeptide it encodes, useful for making
XX PT transgenic plants with improved characteristics.
XX
XX Claim 2; SEQ ID NO 1901; 612pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule modifying
XX CC plant phenotypes and characteristics, comprising a nucleotide sequence
XX CC that encodes an amino acid sequence exhibiting at least 85% sequence
XX CC identity to an amino acid sequence in the sequence listing or in the
XX CC ortholog alignments of Figure 1, a nucleic acid, which is a complement of
XX CC (a), a nucleic acid, which is the reverse of the nucleotide sequence in
XX CC (a) such that the reverse nucleotide sequence has a sequence order which
XX CC is the reverse of the sequence order of (a) or a nucleic acid capable of
XX CC hybridizing (a-c), under conditions that permit formation of a nucleic
XX CC acid duplex at a temperature of 40-48 degrees C below the melting
XX CC temperature of the nucleic acid duplex. Also included are a vector
XX CC construct (comprising a first nucleic acid having a regulatory sequence
XX CC capable of causing transcription and/or translation in a plant, operably
XX CC linked to a second nucleic acid having the sequence of the isolated
XX CC nucleic acid molecule), a host cell comprising the isolated nucleic acid
XX CC molecule that is flanked by exogenous sequence, a host cell comprising
XX CC the vector construct, an isolated polypeptide comprising an amino acid
XX CC sequence exhibiting at least 85% sequence identity to those cited above,
XX CC introducing an isolated nucleic acid into a host cell, transforming a
XX CC host cell, detecting a nucleic acid in a sample, a host cell or organism
XX CC comprising the nucleic acid molecule, a plant generated from the plant
XX CC cell or seed, a plant (plant cell, plant material or seed) comprising the
XX CC nucleic acid molecule (where the plant has improved characteristics as
XX CC compared to a wild type plant), improving plant characteristics in a
XX CC plant comprising transforming the plant with the nucleic acid sequence,
XX CC and a transgenic plant having a gene construct (comprising the nucleic
XX CC acid encoding a component operably linked to a plant promoter so that the
XX CC component is ectopically overexpressed in the transgenic plant). The
XX CC transgenic plant exhibits faster rate of growth, greater fresh of dry
XX CC weight of maturation, greater fruit or seed yield, higher tolerance to
XX CC pH, higher tolerance to low phosphate concentration, or higher tolerance
XX CC to low nitrogen concentration than a progenitor plant, which does not
XX CC contain the progenitor construct, when the transgenic plant and
XX CC progenitor plant are cultivated under identical environmental conditions,
XX CC where the component is any one of the polypeptides cited above. The
XX CC nucleic acid molecules are useful for producing transgenic plants with
XX CC improved characteristics. The present sequence is a plant nucleic acid
XX CC (cDNA) of the invention.
XX
XX Sequence 565 BP; 210 A; 99 C; 108 G; 148 T; 0 U; 0 Other;
SQ
Query Match 3.8%; Score 18; DB 15; Length 565;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 397 TGTGTTTGGAGTTCTTCAA 414
|||||
DB 57 TGTGTTTGGAGTTCTTCAA 40
RESULT 14
AAH12181/c
ID AAH12181 standard; cDNA; 575 BP.
XX
XX AAH12181;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human cDNA clone (3'-primer) SEQ ID NO:9016.

XX
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX OS Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
XX PR 27-AUG-1999; 99JP-00300253.
XX PR 11-JAN-2000; 2000JP-00118776.
XX PR 02-MAY-2000; 2000JP-00183767.
XX PR 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX PA
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX PT length cDNAs defined in the specification, and for the detection and/or
XX PT diagnosis of the abnormality of the proteins encoded by the full-length
XX PT cDNAs.
XX
XX Claim 3; SEQ ID NO 9016; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX CC length cDNAs defined in the specification. Where a primer set comprises:
XX CC (a) an oligo-dT primer and an oligonucleotide complementary to the
XX CC complementary strand of a polynucleotide which comprises one of the 5602
XX CC nucleotide sequences defined in the specification, where the
XX CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX CC of an oligonucleotide comprising a sequence complementary to the
XX CC complementary strand of a polynucleotide which comprises a 5'-end
XX CC sequence and an oligonucleotide comprising a sequence complementary to a
XX CC polynucleotide which comprises a 3'-end sequence, where the
XX CC oligonucleotide comprises at least 15 nucleotides and the combination of
XX CC the 5'-end sequence/3'-end sequence is selected from those defined in the
XX CC specification. The primer sets can be used in antisense therapy and in
XX CC gene therapy. The primers are useful for synthesizing polynucleotides,
XX CC particularly full-length cDNAs. The primers are also useful for the
XX CC detection and/or diagnosis of the abnormality of the proteins encoded by
XX CC the full-length cDNAs. The primers allow obtaining of the full-length
XX CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
XX CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX CC oligonucleotides, all of which are used in the exemplification of the
XX CC present invention
XX
XX Sequence 575 BP; 184 A; 104 C; 124 G; 155 T; 0 U; 8 Other;
SQ
Query Match 3.8%; Score 18; DB 4; Length 575;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 TGATGTTTCTTCTCAAC 348
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DB 90 TGATGTTTCTTCTCAAC 73
RESULT 15
AAA70256
ID AAA70256 standard; DNA; 675 BP.
XX
XX AAA70256;
XX
XX 07-NOV-2000 (first entry)
XX
XX

us-10-764-316-5.olig.rng

Mon Nov 6 11:55:53 2006

Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:389.
Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
antimalarial; malaria; protozoacide; infection; insecticide; ds.

Plasmodium falciparum.

WO200025728-A2.

11-MAY-2000.

05-NOV-1999; 99WO-US026796.

05-NOV-1998; 98US-0107131P.

(HOFF/) HOFFMAN S.

(CARU/) CARUCCI D.

(GARD/) GARDNER M.

(VENT/) VENTER J C.

Hoffman S, Carucci D, Gardner M, Venter JC;

WPI; 2000-365347/31.

Proteins encoded by chromosome 2 of the human malarial parasite,

Plasmodium falciparum, useful as antimalarial vaccines and in the

diagnosis of P.falciparum infection.

Disclosure; Page 564; 577pp; English.

The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (i) nucleotide sequences (ii) encoding (i); and (2) vaccines against P. falciparum infection comprising (i) or (ii). (i) and (ii) are useful for the development of vaccines against P. falciparum infection. (i) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (i), are useful in the detection of infection with P. falciparum. Furthermore, (i) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification

XX SQ Sequence 675 BP; 300 A; 71 C; 91 G; 213 T; 0 U; 0 Other;

Query Match 3.8%; Score 18; DB 3; Length 675;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAAATAATGGAACACA 19

Db 625 GAAATAATGGAACACA 642

Search completed: November 3, 2006, 20:46:05

Job time : 279.593 secs

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362 AATCGGGCGTGGATTCAGGAGCAATTTGTAATAGTGTGTTTGGCTTCTTCAACAGACAA 421
1140 AATCGGGCGTGGATTCAGGAGCAATTTGTAATAGTGTGTTTGGCTTCTTCAACAGACAA 1199
422 ACGGATCCTTATAGACAGGCCCGCTAACTGGATGATTGACAGGAGATTT 468
1200 ACGGATCCTTATAGACAGGCCCGCTAACTGGATGATTGACAGGAGATTT 1246

RESULT 2
ECCDTABC 2305 bp DNA linear BCT 29-JAN-1999
LOCUS Escherichia coli B6468/62 (O86:H34) cytolethal distending toxin
DEFINITION (cdta, cdtB, cdtC) genes, complete cds.
U03293
VERSION U03293.1 GI:416213
ACCESSION
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

REFERENCE 1 (bases 1 to 2305)
AUTHORS Scott, D.A. and Kaper, J.B.
TITLE Cloning and sequencing of the genes encoding Escherichia coli
cytolethal distending toxin
JOURNAL Infect. Immun. 62 (1), 244-251 (1994)
PUBMED 8262635
AUTHORS Scott, D.A.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-1993) Scott D.A., University of Maryland School
of Medicine, Geographic Med., Center for Vaccine Dev., 10 South
Pine Street, Baltimore, MD 21201, USA

FEATURES
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CDS
99.8%; Score 467; DB 15; Length 1991;
Query Match 100.0%; Pred. No. 1.5e-291;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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780 GAAATAAATGGAACACACATGTCGACAACTTGTTACGGGAGGTGGTCTGTTGATATC 839
62 CTGATGGTTCAGGAGCAGGCGGACGATCCAGCTTCTGCAACGTTGACTGAGCAGCAATTT 121
840 CTGATGGTTCAGGAGCAGGCGGACGATCCAGCTTCTGCAACGTTGACTGAGCAGCAATTT 899
122 AGCACTCCTGGTATTCGATGAATAGTATATCTGGAATAACCGGAACCAATAGTCGCCCA 181
900 AGCACTCCTGGTATTCGATGAATAGTATATCTGGAATAACCGGAACCAATAGTCGCCCA 959
182 CAGGAGTGTGTTATATTTCTACCGTGTGTTGATGCTTCCCTAACAGAGTAAATCTTGGC 241
960 CAGGAGTGTGTTATATTTCTACGTTGTTGATGCTTCCCTAACAGAGTAAATCTTGGC 1019
242 ATTGTTTCAACAGAGAGCTGATGAGGTGATGATGATGATGATGATGATGATGATGATGAT 301
1020 ATTGTTTCAACAGAGAGCTGATGAGGTGATGATGATGATGATGATGATGATGATGATGAT 1079
302 CGACCGATCATCGGCATAGGATGTAATGATGATGATGATGATGATGATGATGATGATGATG 361

gene
CDS

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ORIGIN

Query Match 99.8%; Score 467; DB 15; Length 2305;
Best Local Similarity 100.0%; Pred. No. 1.5e-291;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAATAAATGGAACACACATGTCGACAACTTTGTACGGGAAGTGTCTGTGTATC 61
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QY 62 CTGATGGTTTCAGGAGCGGGCAGTACCACTTCTGCAACGTTGACTGAGCGAGAAATTT 121
Db 1079 CTGATGGTTTCAGGAGCGGGCAGTACCACTTCTGCAACGTTGACTGAGCGAGAAATTT 1138

QY 122 AGCACTCTCGTATTCGGATGAATGAGTATATCTGGAATACCGGAACCAATAGTCGCCCA 181
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QY 182 CAGGAGTTGTTTATATTTCTCACGTTGTGATGCAATTCGCTAACAGAGTAAATCTTGGC 241
Db 1199 CAGGAGTTGTTTATATTTCTCACGTTGTGATGCAATTCGCTAACAGAGTAAATCTTGGC 1258

QY 242 ATTTGTTTCAACAGAGAGCTGATGAGTGAATTTGATATACCTCTCAACTGTTGTATCA 301
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QY 302 CGACCGATCATCGCATAGAAATGGTAATGTTTCTCTCAACCCATGATGGCG 361
Db 1319 CGACCGATCATCGCATAGAAATGGTAATGTTTCTCTCAACCCATGATGGCG 1378

QY 362 AATCGGGCGTGGATTCAGGAGCAATTTGTAATAGTGTGTTTTCAGTCTTCAACAGACAA 421
Db 1379 AATCGGGCGTGGATTCAGGAGCAATTTGTAATAGTGTGTTTTCAGTCTTCAACAGACAA 1438

QY 422 ACGGATCCTATAGACAGCGCGCTAACTGATGATTCAGGAGATTT 468
Db 1439 ACGGATCCTATAGACAGCGCGCTAACTGATGATTCAGGAGATTT 1485

RESULT 3

AY351905
LOCUS
DEFINITION
Escherichia coli strain VTE1456 cytolethal distending toxin (cdtB)
gene, partial cds.

ACCESSION
VERSION
KEYWORDS
SOURCE

AY351905.1 GI:34101070
Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

REFERENCE
AUTHORS
Pandey, M., Khan, A., Das, S.C., Sarkar, B., Kahali, S., Chakraborty, S.,
Chattopadhyay, S., Yamasaki, S., Takeda, Y., Nair, G.B. and
Ramamurthy, T.

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Association of Cytolethal Distending Toxin Locus cdtB with
Enteropathogenic Escherichia coli Isolated from Patients with Acute
Diarrhea in Calcutta, India
J. Clin. Microbiol. 41 (11), 5277-5281 (2003)
14605183
2 (bases 1 to 462)
Pandey, M., Khan, A., Das, S.C., Sarkar, B., Kahali, S., Chakraborty, S.,
Chattopadhyay, S., Yamasaki, S., Takeda, Y., Nair, G.B. and
Ramamurthy, T.

TITLE

JOURNAL
SUBMITTED (23-JUL-2003) Microbiology, National Institute of Cholera
and Enteric Diseases, P-33, CIT Road, Scheme, XM, Beliaghata,
Calcutta, West Bengal 700010, India

FEATURES

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Gene

CDS

ORIGIN

Query Match 98.7%; Score 462; DB 15; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.5e-286;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAATAAATGGAACACACATGTCGACAACTTTGTACGGGAAGTGTCTGTGTATC 61
Db 1 GAAATAAATGGAACACACATGTCGACAACTTTGTACGGGAAGTGTCTGTGTATC 60

QY 62 CTGATGGTTTCAGGAGCGGGCAGTACCACTTCTGCAACGTTGACTGAGCGAGAAATTT 121
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QY 122 AGCACTCTCGTATTCGGATGAATGAGTATATCTGGAATACCGGAACCAATAGTCGCCCA 181
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QY 242 ATTTGTTTCAACAGAGAGCTGATGAGTGAATTTGTAATACCTCTCAACTGTTGTATCA 301
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QY 362 AATCGGGCGTGGATTCAGGAGCAATTTGTAATAGTGTGTTTTCAGTCTTCAACAGACAA 421
Db 361 AATCGGGCGTGGATTCAGGAGCAATTTGTAATAGTGTGTTTTCAGTCTTCAACAGACAA 420

QY 422 ACGGATCCTATAGACAGCGCGCTAACTGATGATTCAGGAGATTT 463
Db 421 ACGGATCCTATAGACAGCGCGCTAACTGATGATTCAGGAGATTT 462

RESULT 4
AY351906
LOCUS

AY351906 462 bp DNA linear BCT 07-NOV-2003

```

DEFINITION Escherichia coli strain GB1807 cytolethal distending toxin (cdtB)
ACCESSION AY351906
VERSION AY351906.1 GI:34101072
KEYWORDS
SOURCE
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE
AUTHORS Pandey,M., Khan,A., Das,S.C., Sarkar,B., Kahali,S., Chakraborty,S.,
Chattopadhyay,S., Yamasaki,S., Takeda,Y., Nair,G.B. and
Ramamurthy,T.
TITLE Association of Cytolethal Distending Toxin Locus cdtB with
Enteropathogenic Escherichia coli Isolated from Patients with Acute
Diarrhea in Calcutta, India
J. Clin. Microbiol. 41 (11), 5277-5281 (2003)
14605183
JOURNAL
PUBMED
AUTHORS Pandey,M., Khan,A., Das,S.C., Sarkar,B., Kahali,S., Chakraborty,S.,
Chattopadhyay,S., Yamasaki,S., Takeda,Y., Nair,G.B. and
Ramamurthy,T.
TITLE Direct Submission
Submitted (24-JUL-2003) Microbiology, National Institute of Cholera
and Enteric Diseases, P-33, CIT Road, Scheme, XM, Beliaghata,
Calcutta, West Bengal 700010, India
Location/Qualifiers
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ORIGIN
Query Match 98.7%; Score 462; DB 15; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.5e-288;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAATAAATGGAACACACATGTCGACAACTTGTTACGGGAAGTGGTCTGTGTATATC 61
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QY 422 ACGGATCCTATAAGACAGAGCGCGCTAACTGGATGATTCAGGA 463
DB 421 ACGGATCCTATAAGACAGAGCGCGCTAACTGGATGATTCAGGA 462

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DEFINITION Escherichia coli strain GB1371 cytolethal distending toxin (cdtB)
ACCESSION AY351907
VERSION AY351907.1 GI:34101074
KEYWORDS
SOURCE
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE
AUTHORS Pandey,M., Khan,A., Das,S.C., Sarkar,B., Kahali,S., Chakraborty,S.,
Chattopadhyay,S., Yamasaki,S., Takeda,Y., Nair,G.B. and
Ramamurthy,T.
TITLE Association of Cytolethal Distending Toxin Locus cdtB with
Enteropathogenic Escherichia coli Isolated from Patients with Acute
Diarrhea in Calcutta, India
J. Clin. Microbiol. 41 (11), 5277-5281 (2003)
14605183
JOURNAL
PUBMED
AUTHORS Pandey,M., Khan,A., Das,S.C., Sarkar,B., Kahali,S., Chakraborty,S.,
Chattopadhyay,S., Yamasaki,S., Takeda,Y., Nair,G.B. and
Ramamurthy,T.
TITLE Direct Submission
Submitted (25-JUL-2003) Microbiology, National Institute of Cholera
and Enteric Diseases, P-33, CIT Road, Scheme, XM, Beliaghata,
Calcutta, West Bengal 700010, India
Location/Qualifiers
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ORIGIN
Query Match 98.7%; Score 462; DB 15; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.5e-288;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAATAAATGGAACACACATGTCGACAACTTGTTACGGGAAGTGGTCTGTGTATATC 61
DB 1 GAAATAAATGGAACACACATGTCGACAACTTGTTACGGGAAGTGGTCTGTGTATATC 60
QY 62 CTGATGGTTTCAGAGGCGAGGCGAGTACCAGCTTCTGCAACGTTGACTGACGCGAGAATTT 121
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Qy	422	ACGGATCTCTATAAGACAGCGCGCTAACTGGATGATTGCAGGA	463
Db	421	ACGGATCTCTATAAGACAGCGCGCTAACTGGATGATTGCAGGA	462
RESULT 6			
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LOCUS	AY426341	494 bp	DNA
DEFINITION	Escherichia coli 3015-99 cytolethal distending toxin B subunit (cdtB) gene, partial cds.		linear
ACCESSION	AY426341		BCT 27-JAN-2004
VERSION	AY426341.1		
			GI:37575478

RESULT 6	AY426341	494 bp	DNA	linear	BCT 27-JAN-2004
LOCUS	AY426341				
DEFINITION	Escherichia coli 3015-99 cytolethal distending toxin B subunit (CdtB) gene, partial cds.				
ACCESSION	AY426341				
VERSION	AY426341.1				GT:37575478

ANIMORPHS	SOURCE	ORGANISM
1		<i>Escherichia coli</i>
2		<i>Escherichia coli</i>
3		Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Escherichia</i> .

REFERENCE
AUTHORS
TITLE
JOURNAL

14742509
2 (bases 1 to 494)
Pickett, C.L., Lee, R.B., Eyigor, A., Elitzur, B., Fox, E.M. and
Strockbine, N.A.
Direct Submission
Submitted (01-OCT-2003) Microbiology, Immunology, and Molecular
Genetics, University of Kentucky, 800 Rose Street, Lexington, KY
40536, USA

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ANNM"

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ORIGIN

Query Match 64.5%; Score 302; DB 15; Length 494;
Best Local Similarity 99.3%; Pred. No. 4.le-184;

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Qy	62	CTGATGGTTCAGGAGGACGGGGCAGTACCAAGCTTCTGCAACGTTGACTGAGCGAGAAATTT	121						
Db	100	CTGATGGTTCAGGAGGACGGGGCAGTACCAAGCTTCTGCAACGTTGACTGAGCGAGAAATTT	159						
Qy	122	AGCACTCTGGTATTCGGATGAATGAGTATATCTGGAATACCGGAACCAATAGTCGCCCA	181						
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TITLE	Enterobacteriaceae; Escherichia.								
JOURNAL	1 (bases 1 to 463)								
PUBMED	Bouzari.S., Oloomi,M. and Oswald,E.								
AUTHORS	Detection of the cytolethal distending toxin locus cdtB among								
TITLE	diarrhegenic Escherichia coli isolates from humans in Iran								
JOURNAL	Res. Microbiol. 156 (2), 137-144 (2005)								
FEATURES	15748977								
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gene	Bouzari.S., Oloomi,M. and Zarepoor,M.								
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AUTHORS		Purdy,D.M., Charlton,S.M. and Henderson,I.D.	
TITLE		Use of lytic toxins and toxin conjugates	
JOURNAL		Patent: WO 0134205-A 3 17-MAY-2001;	
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	417 bp DNA linear BCT 05									

Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: zfish-help@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

En: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep

Clone-derived zebrafish pUC subclones occasionally display

inconsistency over the length of mononucleotide A/T runs and

conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Any regions longer than 1kb tagged as misc-feature 'unaura' are

part of a tandem repeat of more than 10kb in length where it has

not been possible to anchor the base differences between repeat

copies. The region has been built up based on the repeat element

to match the total size of repeat indicated by restriction digest,

but repeat copies may not be in the correct order and the usual

finishing criteria may not apply.

DKEY-263L8 is from a Zebrafish BAC library

VECTOR: pindigoBAC-5.

Location/Qualifiers

1. 136195

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FEATURES

source

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Db 95145 TTTTGAGTCTTCAACAGACA 95125

RESULT 13

AC128885

LOCUS

DEFINITION

AC128885

AC128885.3 GI:25139458

HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.

KEYWORDS

SOURCE

ORGANISM

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gregorogis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuewa, L., Loulseghe, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mahoney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidas, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwokedemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villanana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, R., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleciyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 141587)

Worley, K.C.

Direct Submission

JOURNAL

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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Center: Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: KAXT

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Human Genome Sequencing Consortium

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Human Genome Sequencing Consortium

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Human Genome Sequencing Consortium

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Center clone name: CH230-334P14
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Assembly program: Phrap; version 0.990329
Consensus quality: 127509 bases at least Q40
Consensus quality: 130224 bases at least Q30
Consensus quality: 131369 bases at least Q20
Estimated insert size: 129726; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
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* 105420 105519: gap of unknown length
* 105520 138656: contig of 33137 bp in length
* 138657 138756: gap of unknown length
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Matches 21; Conservative 0; Mismatches 0;

QY 388 TGTAAATAGTGTGTTTGAGTT 408
Db 84315 TGTAAATAGTGTGTTTGAGTT 84335

RESULT 14
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LOCUS Bos taurus clone CH240-245G12, *** SEQUENCING IN PROGRESS ***, 29
DEFINITION unordered pieces.
AC175073
ACCESSION AC175073.2 GI:86200618
VERSION AC175073.2
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 191669)
Muzny D., Adams C., Agbai II.O., Allen C., Alsbrooks S., Archer P.,
Aredondo H., Bandaranaike D., Bangura L., Beltran B., Beltran R.,
Beraducci A., Biswal K., Blyth P., Bonham H., Buhay C., Burch P.,
Cadoree I., Canada A., Cardenas V., Carter K., Cavazos I.,
Chacko J., Chahrour M., Chavez D., Chen A., Chen G., Chen R.,
Cheng M.-T., Chu J., Clerc K., Cockrell R., Coyle M., Cree A.,
Curry S., Dai W., Davila M.L., Davis C., Davy-Carroll L., De
Anda C., Delgado O., Denson S., Deramo C., Ding Y., Dinh H.,
Donlin J., McCauley S., Dugan-Rocha S., Dunn A., Durbin K.,
Dziuda D., Egan A., Escotto M., Espinosa V., Eugene C., Fa M.,
Fernandez S., Fernando P., Flagg N., Forbes L., Foster P.,
Fowler G., Fu Q., Fuh E., Garcia A., Garcia R., Garner T.,
Gaiklin C., Gench S., Ghose S., Gill R., Gonzalez D.,
Gonzalez-Garay M., Guevara W., Holder M., Haaland W., Haerberlen K.,
Hall B., Hamid H., Hamilton K., Harbes B., Harris R., Havlak P.,
Hawes A., Hawkins E., Hayes S., Hemphill L., Hernandez J.,
Hines S., Hitchens M., Hodgson A., Hogues M., Hollins B.,
Howell L.T., Hulyk S., Hume J., Imo K., Jackson A., Jackson L.,
Jacob L., Jhang H., Johnson B., Johnson R., Kalatus K., Kelly S.,
Keys T., Khan Z., King L., Kovar C., Kowis A., Kowis C., Lara F.,
Leal S., Lee K., Lee S., LeGall P.I., Lemon S., Lewis L., Li B.,
Li Y., Li Z., Linnell M., Liu W., Liu Y.-S., Liu Y., Liyanage D.,
London P., Lopez J., Lorensuhsela L., Lozada R., Luk T., Madu R.,
Maheshwari M., Mahoney C., Malloy K., Mancouri D., Martinez E.,
McClallan H., McPherson J., Mercadado C., Metzger M.,
Milosavljevic A., Minja E., Morgan M., Morris S., Munidasa M.,
Murray D., Nazareth L., Ngo D., Nguyen N., Norwig-Eastaugh E.,
Nott A., Nwaokemele O., Obregon M., Ochi-Okorie C., Odeh E.,
Okwuonu G., Okwuonu K., Parker D., Pasternak S., Patel B.,
Patel V., Paul H., Perez A., Perez L., Petrosino J., Pham T.,
Primus E., Pu L.-L., Puazo M., Qin X., Quinn A., Quiroz J.,
Rabata D., Rachlin E., Reigh R., Ren Y., Reuter M., Richards S.,
Rives C., Rodriguez F., Rojas A., Ruiz S.J., Sana M., Sanders W.,
Santibanez J., Santos R., Savary G., Scherer S., Shen H., Shen Y.,
Sisson I., Sneed A., Sodergren E., Song X.-Z., Sorelle R.,
Svatek A., Taylor E., Taylor T., Thomas N., Thorn R., Thornton R.,
Trejos Z., Uemami K., Vargo C., Verduzco D., Villasana D., Virk D.,
Volkov A., Waldron L., Walker B., Wang O., Wang S., Warren J.,
Wei X., Wheeler D., Williams G., Williams R., Worley K., Wright R.,
Wu J., Yakub S., Yan K., Yuan Y., Yu F., Zhang J., Zhang L.,
Zhang Z., Zhou J., Weinstein G. and Gibbs R.A.
Direct Submission
Unpublished
2 (bases 1 to 191669)
Worley K.C.
Direct Submission
Submitted (06-JAN-2006) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 191669)

Bovine Genome Sequencing Consortium
Direct Submission
Submitted (31-JAN-2006) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jan 31, 2006 this sequence version replaced gi:84490450.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: FNEW
Center clone name: CH240-245G12
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 169512 bases at least Q40
Consensus quality: 171717 bases at least Q30

```

Consensus quality: 173988 bases at least Q20
Estimated insert size: 175814; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1361: contig of 1361 bp in length
* 1362 2075: gap of 714 bp
* 2076 6680: contig of 4605 bp in length
* 6681 6780: gap of unknown length
* 6781 11436: contig of 4656 bp in length
* 11437 12103: gap of 667 bp
* 12104 13463: contig of 1360 bp in length
* 13464 13670: gap of 207 bp
* 13671 17094: contig of 3424 bp in length
* 17095 17503: gap of 409 bp
* 17504 21392: contig of 3889 bp in length
* 21393 21492: gap of unknown length
* 21493 36367: contig of 14875 bp in length
* 36368 36417: gap of 50 bp
* 36418 42996: contig of 6579 bp in length
* 42997 43046: gap of 50 bp
* 43047 55330: contig of 12284 bp in length
* 55331 57120: contig of 1740 bp in length
* 57121 65692: gap of 8572 bp
* 65693 68984: contig of 3292 bp in length
* 68985 69034: gap of 50 bp
* 69035 71002: contig of 1968 bp in length
* 71003 71052: gap of 50 bp
* 71053 77566: contig of 6514 bp in length
* 77567 78438: gap of 872 bp
* 78439 82513: contig of 4075 bp in length
* 82514 82563: gap of 50 bp
* 82564 92873: contig of 10260 bp in length
* 92874 96190: contig of 3317 bp in length
* 96191 96240: gap of 50 bp
* 96241 99785: contig of 3545 bp in length
* 99786 100387: gap of 602 bp
* 100388 108057: contig of 7670 bp in length
* 108058 120856: contig of 12749 bp in length
* 120857 120906: gap of 50 bp
* 120907 126815: contig of 5909 bp in length
* 126816 126865: gap of 50 bp
* 126866 133104: contig of 6239 bp in length
* 133105 133204: gap of unknown length
* 133205 161407: contig of 28203 bp in length
* 161408 161457: gap of 50 bp
* 161458 178544: contig of 17087 bp in length
* 178545 178644: gap of unknown length
* 178645 180745: contig of 2001 bp in length
* 180746 181866: contig of 1121 bp in length
* 181867 181967: gap of unknown length
* 181968 183136: contig of 1170 bp in length
* 183137 183236: gap of unknown length
* 183237 184890: contig of 1654 bp in length
* 184891 184990: gap of unknown length
* 184991 187827: contig of 2837 bp in length
* 187828 187927: gap of unknown length
* 187928 191669: contig of 3742 bp in length.
* 191669

Location/Qualifiers
1. .191669

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/db_xref="taxon:9913"
/clone="CH240-245G12"
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Query Match 4.5%; Score 21; DB 12; Length 191669;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 AATTGTAATAGTGTTTTGA 405
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Db 29658 AATTGTAATAGTGTTTTGA 29638

RESULT 15
AC107439/c AC107439 238377 bp DNA linear HTG 19-NOV-2002
LOCUS Rattus norvegicus clone CH230-229M1, *** SEQUENCING IN PROGRESS
DEFINITION *** 8 unordered pieces.
ACCESSION AC107439
VERSION AC107439.5 GI:25075945
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 238377)
REFERENCE
AUTHORS Muzny, D., Marie, J., Metzker, M., Lee, J., Adams, C., Alder, J.,
Allen, C., Allent, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, P.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kratt, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshew, L., Loulaeged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milobavljovic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundaasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polinder, A., Popovic, D., Primus, E., Pu, L., Puzo, M., Quiroz, J., Rachen, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojase, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villana, D., Waldrton, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Woodman, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Smith, H.O., Niederhauser, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 238377)
Worley, K.C.
Direct Submission
Submitted (21-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 238377)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23603151.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GNI
Center clone name: CH230-229M1
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 176033 bases at least Q40
Consensus quality: 178158 bases at least Q30

Consensus quality: 179520 bases at least Q20
Estimated insert size: 178417; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 10410: contig of 10410 bp in length
* 10411 10510: gap of unknown length
* 10511 20957: contig of 10447 bp in length
* 20958 21057: gap of unknown length
* 21058 224179: contig of 203122 bp in length
* 224180 224279: gap of unknown length
* 224280 229532: contig of 5253 bp in length
* 229533 229632: gap of unknown length
* 229633 230665: contig of 1033 bp in length
* 230666 230765: gap of unknown length
* 230766 231997: contig of 1232 bp in length
* 231998 232097: gap of unknown length
* 232098 234781: contig of 2684 bp in length
* 234782 234881: gap of unknown length
* 234882 239377: contig of 3496 bp in length.
Location/Qualifiers
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/db_xref="taxon:10116"
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1..1567
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/note="clone_boundary"
clone_end:Sp6
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/estimated_length=unknown
224280..225441
/notes="wgs_end_extension"
clone_end:Sp6"
229533..229632
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230666..230765
/estimated_length=unknown
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/estimated_length=unknown
234782..234881
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shotgun sequence only contigs will be indicated in the feature table.

Query Match 4.5%; Score 21; DB 12; Length 238377;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 388 TGTAAATAGTCTTTTGAGTT 408
DB 178170 TGTAAATAGTCTTTTGAGTT 178150

Search completed: November 4, 2006, 01:20:27

Job time : 2602.63 secs

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